

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: _____ Examiner #: _____ Date: _____
 Art Unit: _____ Phone Number 30 _____ Serial Number: _____
 Mail Box and Bldg/Room Location: _____ Results Format Preferred (circle): PAPER DISK E-M

If more than one search is submitted, please prioritize searches in order of need.

 Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept of utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Jan Delaval
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	Type of Search	Vendors and cost where applicable
Searcher: <u>Jan</u>	NA Sequence (#) _____	STN _____
Searcher Phone #: <u>4498</u>	AA Sequence (#) <input checked="" type="checkbox"/>	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: <u>2/8/03</u>	Bibliographic _____	Dr.Link _____
Date Completed: <u>2-11-03</u>	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems <input checked="" type="checkbox"/>
Clerical Prep Time: <u>30</u>	Patent Family _____	WWW/Internet _____
Online Time: <u>+ 90</u>	Other _____	Other (specify) _____

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:39:10 ; Search time 13.2 Seconds
(without alignments)
80.112 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KQIKHVKLK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	631	2 JC4298	hyaluronan recepto
2	54	100.0	725	1 JC5016	hyaluronan recepto
3	37	68.5	148	2 T50808	hypothetical prote
4	37	68.5	624	2 H90071	hypothetical prote
5	37	68.5	1473	2 A90116	DNA-directed RNA p
6	37	68.5	1495	2 T48429	hypothetical prote
7	36	66.7	222	2 H82169	phage shock protei
8	36	66.7	623	2 AB1112	transcription anti
9	36	66.7	623	2 A91473	transcription anti
10	36	66.7	785	2 S54016	SOK2 protein - yea
11	36	66.7	835	2 T48260	hypothetical prote
12	36	66.7	1388	2 T30335	KLP2 protein - Alf
13	35	64.8	117	2 H86640	ribonuclease P (EC
14	35	64.8	168	2 B89836	conserved hypotet
15	35	64.8	237	2 S73504	degy protein homol
16	35	64.8	267	2 F90516	esterase/lipase 1
17	35	64.8	272	2 H75219	hypothetical prote
18	35	64.8	393	2 E88931	protein nhr-58 (lm
19	35	64.8	399	2 S30188	probable ribosoma
20	35	64.8	507	2 C88110	proteasin W24E12.1
21	35	64.8	552	2 S49338	transcription fact
22	35	64.8	789	2 S68427	chloride channel p
23	35	64.8	802	2 S68426	chloride channel p
24	35	64.8	2017	1 A36014	myosin heavy chain
25	35	64.8	2057	2 S61477	myosin II heavy ch
26	35	64.8	2339	2 A45597	DNA-directed RNA p
27	34	63.0	153	2 F86331	F6P9.11 protein -
28	34	63.0	207	2 S62034	probable membrane
29	34	63.0	252	2 A64492	loxin sensitivity

30	34	63.0	298	2 G64465	modification methy
31	34	63.0	340	2 G69474	conserved hypotet
32	34	63.0	346	2 I64237	hypothetical prote
33	34	63.0	373	1 S07463	dihydrokaempferol
34	34	63.0	373	2 A97326	exonuclease ABC,
35	34	63.0	376	2 B64508	hypothetical prote
36	34	63.0	384	2 S14450	probable transpos
37	34	63.0	410	1 QXASR1	21S rRNA intron pr
38	34	63.0	481	2 H64583	glutamine syntheta
39	34	63.0	481	2 B71929	glutamine syntheta
40	34	63.0	491	2 T01856	hypothetical prote
41	34	63.0	545	2 S47530	chaperonin groEL -
42	34	63.0	648	2 JC5930	serine/arginine-ri
43	34	63.0	655	2 S45337	serine protein kin
44	34	63.0	684	2 T26930	hypothetical prote
45	34	63.0	693	2 H90486	alpha-glucosidase

ALIGNMENTS

RESULT 1

JC4298
hyaluronan receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Nov-1995 #sequence-revision 08-Feb-1996 #text-change 01-Dec-2000

C:Accession: JC4298; A42925; A41923; S21586

R:Entwistle, J.; Zhang, S.; Yang, B.; Wong, C.; Li, Q.; Hall, C.L.; A. J.; Mowat, M.; Gene 163, 233-238, 1995

A:Title: Characterization of the murine gene encoding the hyaluronan receptor RHAMM.

A:Reference number: JC4298; MUID:96011659; PMID:7590272

A:Accession: JC4298

A:Molecule type: mRNA

A:Residues: 1-631 <ENT>

A:Cross-references: EMBL:X64550

A:Experimental source: 3T3 fibroblast

R:Hardwick, C. 118, 753, 1992

A:Reference number: A42925; MUID:92348516; PMID:1639856

A:Contents: erratum

A:Accession: A42925

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 155-376, 'S', 378-504, 'E', 506-631 <HAR>

A:Cross-references: GB:X64550

A:Note: authors translated the codon AGT for residue 377 as Thr and CTA for residue 5

J:Hardwick, C.; Hoare, K.; Owens, R.; Hohn, H.P.; Hook, M.; Moore, D.; Cripps, V.; Au R. Cell Biol 117, 1343-1350, 1992

A:Title: Molecular cloning of a novel hyaluronan receptor that mediates tumor cell mo

A:Reference number: A41923; MUID:92296990; PMID:1376732

A:Accession: A41923

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 155-376, 'S', 378-504, 'E', 506-507, 'L', 508-630 <HA2>

A:Cross-references: GB:X64550

A:Note: this sequence has been corrected in reference A42925

C:Comment: This protein regulates cell motility and transformation, and focal adhesio

C:Genetics:

A:Gene: rhamm

A:Introns: 20/3: 54/2; 79/2; 137/3; 187/3; 259/2; 382/2; 431/2; 482/2; 515/3; 574/3;

C:Superfamily: hyaluronan receptor

C:Keywords: glycoprotein; receptor

F:260-382/Region: 21 residue repeats

F:516-574/Region: hyaluronan binding #status predicted

F:575-625/Region: hyaluronan binding #status predicted

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #st

Query Match 100.0%; Score 54; DB 2; Length 631;
Best Local Similarity 100.0%; Pred. No. 0.054;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 KQIKHVKLK 11
|||||

Db 556 KOKIKHVKLK 566

RESULT 2
JC5016
hyaluronan receptor - human
C:Species: Homo sapiens (man)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 29-Sep-1999
C:Accession: JC5016
R:Wang, C.; Entwistle, J.; Hou, G.; Li, Q.; Turley, E.A.
Gene 174, 299-306, 1996
A:Title: The characterization of a human RHAMM cDNA: Conservation of the hyaluronan-binding site
A:Reference number: JC5016, MUID:97045829, PMID:8890751
C:Contents: breast
A:Accession: JC5016
A:Molecule type: mRNA
A:Residues: 1-725 <MAN>
A:Cross-references: GB:U29343
A:Note: It is uncertain whether Met-1 or Met-196 is the Initiator
C:Comment: This receptor regulates focal adhesion turnover, and regulates human breast C
C:Genetics:
A:Gene: GDB:HMNR, RHAMM
A:Cross-references: GDB:683209; OMIM:600936
A:Map position: 5q33.2-5qter
C:Superfamily: hyaluronan receptor

Query Match
Best Local Similarity 100.0%; Score 54; DB 1; Length 725;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KOKIKHVKLK 11
|||||

Db 636 KOKIKHVKLK 646

RESULT 3
T50808
hypothetical protein T30N20_260 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: T50808
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.; Mey
submitted to the Protein Sequence Database, July 2000
A:Reference number: 225240
A:Accession: T50808
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-148 <BEV>
A:Cross-references: EMBL:AL365234
A:Experimental source: cultivar Columbia; BAC clone T30N20
C:Genetics:
A:Map position: 5
A:Note: T30N20_260

Query Match
Best Local Similarity 68.5%; Score 37; DB 2; Length 148;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 3 KIKHVKLK 11
|||:

Db 10 KIRHIVKLK 18

RESULT 4
H90071
hypothetical protein SA2433 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H90071
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitsutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C:Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001

A:Title: Whole genome sequencing of melicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H90071
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-624 <KUR>
A:Cross-references: GB:BA000018; PID:g13702598; PIDN:BA843738.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA2433

Query Match
Best Local Similarity 68.5%; Score 37; DB 2; Length 624;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KOKIKHVKLK 11
: |||

Db 464 KHKIRHVKK 474

RESULT 5
A90116
DNA-directed RNA polymerase II largest chain [imported] - *Galliardia theta* nucleomorph
C:Species: nucleomorph *Galliardia theta*
A:Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C:Accession: A90116
R:Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.;
Nature 410, 1091-1096, 2001
A:Title: The highly reduced genome of an enslaved algal nucleus.
A:Reference number: A9082; MUID:11323671; PMID:11323671
A:Accession: A90116
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1473 <DOU>
A:Cross-references: GB:A010592; MUID:g12580785; PIDN:CAC27103.1; GSPDB:GN00151
C:Genetics:
A:Map position: 2
A:Genome: nucleomorph
C:Superfamily: yeast DNA-directed RNA polymerase III 160K chain
C:Keywords: nucleomorph

Query Match
Best Local Similarity 68.5%; Score 37; DB 2; Length 1473;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 2 OKIKHVKLK 11
|||:

Db 112 OKIKHVKLK 121

RESULT 6
T48429
hypothetical protein F8F6_230 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: T48429
R:Bevan, M.; Peters, S.A.; van Staveren, M.; Dirkse, W.; Stiekema, W.; Bancroft, I.;
submitted to the Protein Sequence Database, March 2000
A:Reference number: 224488
A:Accession: T48429
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1495 <BEV>
A:Cross-references: EMBL:AL162873
A:Experimental source: cultivar Columbia; BAC clone F8F6
C:Genetics:
A:Map position: 5
A:Introns: 100/3
A:Note: F8F6_230

Query Match
Best Local Similarity 68.5%; Score 37; DB 2; Length 1495;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOKIKHVVK 9
 |||::|||
 Db 584 KKKVKKLVK 592

RESULT 7
 H82169
 phage shock protein A VC1678 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
 C:Species: Vibrio cholerae
 C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: H82169
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.;
 charadson, D.; Emolaeva, M.D.; Yamathavan, J.; Bass, S.; Olin, H.; Dragol, I.; Sellers, F.
 L.; R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A>Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A:Reference number: AB2035; MUID:20406833; PMID:10952301
 A:Accession: H82169
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-222 <HEI>
 A:Cross-references: GB:AE004246; GB:AE003852; NID:g9656191; PIDN:AAF94828.1; GSPDB:GN001
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC1678
 A:Map position: 1

Query Match 66.7%; Score 36; DB 2; Length 222;
 Best Local Similarity 66.7%; Pred. No. 35;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOKIKHVVK 9
 |||::|||
 Db 94 KOKIKHVVK 102

RESULT 8
 AB1112
 transcription antiterminator (BglG family) homolog lmo0297 [imported] - Listeria monocyt
 C:Species: Listeria monocytogenes
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AB1112
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fshl, H.
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maltournam, A.; Ma
 Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A>Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AB1112
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-623 <GLA>
 A:Cross-references: GB:NC_003210; PIDN:CAD00824.1; PID:g16409662; GSPDB:GN00177
 A:Experimental source: strain ESD-e
 C:Genetics:
 A:Gene: lmo0297

Query Match 66.7%; Score 36; DB 2; Length 623;
 Best Local Similarity 60.0%; Pred. No. 1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 OKIKHVVK 11
 ||||::|
 Db 462 OKIKHLETK 471

RESULT 9
 AF1473
 transcription antiterminator (BglG family) homolog lln0325 [imported] - Listeria innocua

C:Species: Listeria innocua
 C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001
 C:Accession: AF1473
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloec
 .; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entlian, K.D.; Fshl,
 D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapk, G.; Madueno, E.; Maltournam, A.;
 Ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehla
 A>Title: Comparative genomics of Listeria species.
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AF1473
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-623 <GLA>
 A:Cross-references: GB:AL592022; PIDN:CA095558.1; PID:g16412754; GSPDB:GN00178
 A:Experimental source: strain Clp11262
 C:Genetics:
 A:Gene: lln0325

Query Match 66.7%; Score 36; DB 2; Length 623;
 Best Local Similarity 60.0%; Pred. No. 1e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

OY 2 OKIKHVVK 11
 ||||::|
 Db 462 OKIKHLETK 471

RESULT 10
 S54016
 S0K2 protein - yeast (Saccharomyces cerevisiae)
 N:Alternate names: protein YW9711.03c; protein YMR016c
 C:Species: Saccharomyces cerevisiae
 C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 06-Feb-1998
 C:Accession: S54016
 R:Iye, G.; Churcher, C.M.
 submitted to the EMBL data library, May 1995
 A:Reference number: S54014
 A:Accession: S54016
 A:Molecule type: DNA
 A:Residues: 1-785 <YE>
 A:Cross-references: EMBL:249211; NID:g798922; PID:g798925; MIPS:YMR016c
 A:Experimental source: strain AB972
 C:Genetics:
 A:Gene: SGD:S0K2
 A:Cross-references: SGD:S0004618; MIPS:YMR016c
 A:Map position: 13R

Query Match 66.7%; Score 36; DB 2; Length 785;
 Best Local Similarity 66.7%; Pred. No. 1.3e+02;
 Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 OKIKHVVK 10
 |||::|||
 Db 469 EKIRHVVKI 477

RESULT 11
 T48260
 hypothetical protein T1E22.150 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T48260
 R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Bancro
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: 224489
 A:Accession: T48260
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-835 <BEV>
 A:Cross-references: EMBL:AL162874
 A:Experimental source: cultivar Columbia; BAC clone T1E22

C:Genetics:
A:Map position: 5
A:Introns: 53/1: 82/3: 638/1
A:Note: TLE22.150

Query Match
Best Local Similarity 66.7%; Score 36; DB 2; Length 835;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOKIKHV 8
IIIIII
DB 410 KOKIKHVI 417

RESULT 12
T30335
KLP2 protein - African clawed frog
C:Species: Xenopus laevis (African clawed frog)
C:Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 02-Jun-2000
C:Accession: T30335
R:Boletl, H.; Karsenti, E.; Vernos, I.
Cell 84, 49-59, 1996
A:Title: KLP2, a new Xenopus centrosomal kinesin-like protein required for centrosome
A:Reference number: 220827; MUID:96140639; PMID:8548825
A:Accession: T30335
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1388 <BOL>
A:Cross-references: EMBL:X94082; NID:g1129172; PID:e213754; PIDN:CAA63826.1
C:Genetics:
A:Gene: KLP2
C:Superfamily: unassigned kinesin-related proteins; kinesin motor domain homology

Query Match
Best Local Similarity 66.7%; Score 36; DB 2; Length 1388;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 OKIKHVVKLK 11
IIIIII
DB 1349 OKIKVYVKLK 1358

RESULT 13
H86640
ribonuclease P (EC 3.1.26.5) [imported] - Lactococcus lactis subsp. lactis (strain IL140
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 03-Aug-2001
C:Accession: H86640
R:Boletl, A.; Wincker, P.; Manger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: H86640
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-117 <STO>
A:Cross-references: GB:AE005176; PID:g12722976; PIDN:AAK04226.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: rnpA
C:Keywords: hydrolase

Query Match
Best Local Similarity 64.8%; Score 35; DB 2; Length 117;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOKIKHVVKL 10
II:IIII:II
DB 98 KKNLKHVVKL 107

RESULT 14
B89836

conserved hypothetical protein SA0612 [imported] - Staphylococcus aureus (strain N315
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: B89836
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; O
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sano, T.; Inoue, R.; Kaito, C.; Sekimizu, K
C.; Shibata, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89836
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-168 <KUR>
A:Cross-references: GB:BA000018; PID:g13700548; PIDN:BA841845.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0612

Query Match
Best Local Similarity 64.8%; Score 35; DB 2; Length 168;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 OKIKHVVKL 10
I:IIII I:
DB 80 OKIKHVAKI 88

RESULT 15
S73504
degV protein homolog K05_orf237 - Mycoplasma pneumoniae (strain ATCC 29342)
C:Species: Mycoplasma pneumoniae
A:Variety: ATCC 29342
C:Date: 27-Feb-1997 #sequence_revision 25-Apr-1997 #text_change 07-Dec-1999
C:Accession: S73504
R:Himmelreich, R.; Hilbert, H.; Plagens, H.; Pirkl, E.; Li, B.C.; Herrmann, R.
Nucleic Acids Res. 24, 4420-4449, 1996
A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumon
A:Reference number: S73327; MUID:97105885; PMID:8948633
A:Accession: S73504
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-237 <HIM>
A:Cross-references: EMBL:AE000019; GB:U00089; NID:g1673839; PIDN:AA895826.1; PID:g167
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
C:Genetics:
A:Genetic code: SGC3

Query Match
Best Local Similarity 64.8%; Score 35; DB 2; Length 237;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOKIKHVVKLK 11
II:IIII
DB 171 KOLKHSVKLK 181

Search completed: February 8, 2003, 10:43:24
Job time : 15.2 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:36:15 ; Search time 6.96667 Seconds
(without alignments)
65.489 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KOKIKHVKLK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	54	100.0	498 1 HMMR_RAT	P97779 ratius norv
2	54	100.0	724 1 HMMR_HUMAN	O75330 homo sapien
3	54	100.0	794 1 HMMR_MOUSE	O00547 mus musculu
4	36	66.7	785 1 SOR2_YEAST	P53438 saccharomyc
5	35	64.8	117 1 RNPA_LACLA	O9C173 lactococcu
6	35	64.8	237 1 Y450_MYCPN	P75127 mycoplasma
7	35	64.8	399 1 RMS5_PENUR	P47907 penicillium
8	35	64.8	552 1 EFG1_CANAL	P43064 candida alb
9	35	64.8	803 1 CLC7_MOUSE	O70496 mus musculu
10	35	64.8	803 1 CLC7_RAT	P51789 ratius norv
11	35	64.8	805 1 CLC7_HUMAN	P51798 homo sapien
12	35	64.8	2017 1 MYSN_DROME	O99323 drosophila
13	35	64.8	2339 1 RPCI_PLAFA	P27625 plasmodium
14	34	63.0	196 1 PER1_HUMAN	O15288 homo sapien
15	34	63.0	298 1 MTM4_METJA	O58274 methanococc
16	34	63.0	340 1 Y100_AKFU	O28474 archaeoglob
17	34	63.0	346 1 Y343_MYCGE	P47565 mycoplasma
18	34	63.0	380 1 DFRA_PETHY	P14720 petunia hyb
19	34	63.0	410 1 RMS5_EMENT	P02382 emeticella
20	34	63.0	481 1 GLNA_HELPJ	O92145 helicobacte
21	34	63.0	481 1 GLNA_HELPY	P94845 helicobacte
22	34	63.0	545 1 CH60_PORGI	P42375 porphyromon
23	34	63.0	693 1 AGLO_SULOS	O59645 sulfolobus
24	34	63.0	747 1 DIL2_HUMAN	O91400 homo sapien
25	33	61.1	63 1 RL30_RICPR	O92C83 rickettsia
26	33	61.1	286 1 TYSY_BPT4	P00471 bacterioph
27	33	61.1	312 1 EBP2_XENLA	O91816 xenopus lae
28	33	61.1	330 1 PHUC_STRAU	P09978 staphylococ
29	33	61.1	374 1 CATB_PSEPU	P08310 pseudomonas
30	33	61.1	426 1 GSA_THBAC	O9hk06 thermoplasm
31	33	61.1	481 1 ALGA_PSEAE	P07874 p alginata
32	33	61.1	515 1 MATK_CEDAT	O9mv56 cedrus atla
33	33	61.1	572 1 GPC5_HUMAN	P78333 homo sapien

34	33	61.1	584 1 LMRA_LACLC	P97046 lactococcus
35	33	61.1	611 1 PEPR_MYCPN	P54125 mycoplasma
36	33	61.1	665 1 PD12_RAT	P20717 ratius norv
37	33	61.1	673 1 PD12_MOUSE	O08642 mus musculu
38	33	61.1	809 1 LEF_BACAN	P15917 bacillus an
39	33	61.1	2005 1 CIN2_RAT	P04775 ratius norv
40	33	61.1	2009 1 CINI_HUMAN	P35498 homo sapien
41	33	61.1	3210 1 CENF_HUMAN	P49454 homo sapien
42	32	59.3	50 1 R331_MYCPN	O98477 mycoplasma
43	32	59.3	119 1 RNPA_STRPY	O9a114 streptococc
44	32	59.3	136 1 YM33_MARPO	P38475 marchantia
45	32	59.3	146 1 YAN3_SCHPO	O10069 schizosacch

ALIGNMENTS

RESULT 1
HMMR_RAT
ID HMMR_RAT STANDARD; PRT; 498 AA.
AC P97779;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE Hyaluronan mediated motility receptor (intracellular hyaluronan acid binding protein) (Receptor for hyaluronan-mediated motility).
GN HMMR OR IHABP OR RHAMM.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
ON NCBI_TaxID=10116;
RX [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vascular smooth muscle;
RA Savani R.C., Hou G.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: INVOLVED IN CELL MOTILITY. WHEN HYALURONAN BINDS TO HMMR, THE PHOSPHORYLATION OF A NUMBER OF PROTEINS, INCLUDING THE FOCAL ADHESION KINASE OCCURS. MAY ALSO BE INVOLVED IN CELLULAR TRANSFORMATION AND METASTASIS FORMATION, AND IN REGULATING EXTRACELLULAR-REGULATED KINASE (ERK) ACTIVITY (BY SIMILARITY).
CC -!- SUBUNIT: SUBUNIT OF THE HARC COMPLEX.
CC -!- SUBCELLULAR LOCATION: CELL SURFACE AND CYTOPLASMIC (BY SIMILARITY).
CC -----
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CC -----
DR EMBL: U87983; AAB47997.1; -
KW Hyaluronan acid; Receptor; Glycoprotein.
FT DOMAIN 420 430
FT DOMAIN 442 451
FT CARBOHYD 262 262
FT CARBOHYD 302 302
FT CARBOHYD 483 483
SQ SEQUENCE 498 AA; 5785 MW; 58037C79B5DC2A70 CRC64;
Query Match 100.0%; Score 54; DB 1; Length 498;
Best local Similarity 100.0%; Pred. No. 0.012;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KOKIKHVKLK 11
IIIIIIIIIIII
Db 420 KOKIKHVKLK 430
RESULT 2
HMMR_HUMAN

ID HMWR_HUMAN STANDARD; PRT; 724 AA.
 AC 075330; 092767;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Hyaluronan mediated motility receptor (intracellular hyaluronic acid binding protein) (Receptor for hyaluronan mediated motility) (CD108 antigen).
 GN HMWR OR IHABP OR RHAMM.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Plimates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND CHARACTERIZATION.
 RC TISSUE-Breast carcinoma;
 RX MEDLINE=98264864; Pubmed=9601098;
 RA Assmann V., Marshall J.F., Fleber C., Hofmann M., Hart I.R.;
 RT "The human hyaluronan receptor RHAMM is expressed as an intracellular protein in breast cancer cells."
 RL J Cell Sci. 111:1685-1694(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Breast;
 RX MEDLINE=97045829; Pubmed=8890751;
 RA Wang C., Entwistle J., Hou G., Li Q., Turley E.A.;
 RT "The characterization of a human RHAMM cDNA: conservation of the hyaluronan-binding domains."
 RL Gene 174:299-306(1996).
 CC -1- FUNCTION: INVOLVED IN CELL MOTILITY. WHEN HYALURONAN BINDS TO HMWR, THE PHOSPHORYLATION OF A NUMBER OF PROTEINS, INCLUDING THE FOCAL ADHESION KINASE OCCURS. MAY ALSO BE INVOLVED IN CELLULAR TRANSFORMATION AND METASTASIS FORMATION, AND IN REGULATING EXTRACELLULAR-REGULATED KINASE (ERK) ACTIVITY.
 CC -1- SUBUNIT: SUBUNIT OF THE HARC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: CELL SURFACE AND CYTOPLASMIC (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: A (SHOWN HERE) AND B: ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN BREAST CANCER CELL LINES AND IN NORMAL BREAST TISSUE.
 CC -1- DATABASE: NAME=PROW; NOTE=PROW 2:76-84(2001); WWW="http://www.ncbi.nlm.nih.gov/prov/guide/802868666.g.htm"
 CC -----
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 CC -----
 DR EMBL: AF032862; AAC32548.1;
 DR EMBL: U29343; AAC52049.1;
 DR GenBank: HGNC:5012; HMWR.
 DR MIM: 600936;
 KW Hyaluronan; acid; Alternative splicing; Repeat; Glycoprotein; Antigen.
 FT DOMAIN 635 645
 FT DOMAIN 657 666
 FT CARBOHYD 133 133
 FT CARBOHYD 477 477
 FT CARBOHYD 567 567
 FT CARBOHYD 588 588
 FT VARSPLIC 75 90
 FT CONFLICT 103 103
 FT CONFLICT 277 277
 FT CONFLICT 298 298
 FT CONFLICT 322 322
 FT CONFLICT 330 332
 FT SEQUENCE 724 AA; 84031 MW; EA68AD6D2A626926 CRC64;
 Query Match 100.0%; Score 54; DB 1; Length 724;

Best Local Similarity 100.0%; Pred. No. 0.018;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 KOKIKHYKK 11
 Db 635 KOKIKHYKK 645
 RESULT 3
 HMWR_MOUSE
 ID HMWR_MOUSE STANDARD; PRT; 794 AA.
 AC 000547;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hyaluronan mediated motility receptor (intracellular hyaluronic acid binding protein) (Receptor for hyaluronan-mediated motility).
 GN HMWR OR IHABP OR RHAMM.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
 RC TISSUE-Lung;
 RX MEDLINE=98264863; Pubmed=9601097;
 RA Hofmann M., Fleber C., Assmann V., Goettlicher M., Sleeman J., Plug R., Howells N., von Stein O., Ponta H., Herrlich P.;
 RT "Identification of IHABP, a 95 kDa intracellular hyaluronate binding protein."
 RL J Cell Sci. 111:1673-1684(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Zhao Y., Zhang S., Turley E.;
 RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1-183 FROM N.A., AND TISSUE SPECIFICITY.
 RC STRAIN=129/Sv;
 RX MEDLINE=99107769; Pubmed=9889313;
 RA Fleber C., Plug R., Sleeman J., Dall P., Ponta H., Hofmann M.;
 RT "Characterization of the murine gene encoding the intracellular hyaluronan receptor IHABP."
 RL Gene 226:41-50(1999).
 RN [4]
 RP SEQUENCE OF 164-794 FROM N.A., AND ALTERNATIVE SPLICING.
 RC STRAIN=BALB/c; TISSUE=Fibroblast;
 RX MEDLINE=96011639; Pubmed=7590272;
 RA Entwistle J., Zhang S., Yang B., Wong C., Li Q., Hall C.L., A.J., Nowak M., Greenberg A.H., Turley E.A.;
 RT "Characterization of the murine gene encoding the hyaluronan receptor RHAMM."
 RL Gene 163:233-238(1995).
 RN [5]
 RP SEQUENCE OF 318-794 FROM N.A., AND CHARACTERIZATION.
 RC STRAIN=BALB/c;
 RX MEDLINE=92296930; Pubmed=1376732;
 RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D., Cripps V., Austen L., Nance D.M., Turley E.A.;
 RT "Molecular cloning of a novel hyaluronan receptor that mediates tumor cell motility."
 RL J. Cell Biol. 117:1343-1350(1992).
 RN [6]
 RP CHARACTERIZATION.
 RX MEDLINE=94308286; Pubmed=7518470;
 RA Hall C.L., Wang C., Lange L.A., Turley E.A.;
 RT "Hyaluronan and the hyaluronan receptor RHAMM promote focal adhesion turnover and transient tyrosine kinase activity."
 RL J. Cell Biol. 126:575-588(1994).
 RN [7]
 RP ERK REGULATION, AND SUBCELLULAR LOCATION.
 RX MEDLINE=98225222; Pubmed=9556628;
 RA Zhang S., Chang M.C., Zyika D., Turley S., Harrison R., Turley E.A.;
 RT "The hyaluronan receptor RHAMM regulates extracellular-regulated

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RT kinase."
RL J. Biol. Chem. 273:11342-11348(1998).
RN [8]
RP REVIEW.
RX MEDLINE=99059494; PubMed=9845361;
RA Hofmann M., Asmann V., Fieber C., Sleeman J.P., Moll J., Ponta H.,
RT Hart I.R., Herrlich P.;
RT "Problems with RHAMM: a new link between surface adhesion and
RT oncogenesis?";
RL Cell 95:591-592(1998).
CC -1- FUNCTION: INVOLVED IN CELL MOTILITY. WHEN HYALURONAN BINDS TO
CC HMMR, THE PHOSPHORYLATION OF A NUMBER OF PROTEINS, INCLUDING THE
CC FOCAL ADHESION KINASE OCCURS. MAY ALSO BE INVOLVED IN CELLULAR
CC TRANSFORMATION AND METASTASIS FORMATION, AND IN REGULATING
CC EXTRACELLULAR-REGULATED KINASE (ERK) ACTIVITY.
CC -1- SUBUNIT: SUBUNIT OF THE HARC COMPLEX.
CC -1- SUBCELLULAR LOCATION: CELL SURFACE AND CYTOPLASMIC.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS: RHAMM1A (SHOWN HERE) AND
CC RHAMM1. ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- TISSUE SPECIFICITY: UBQUITOUSLY EXPRESSED.
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CC -----
DR EMBL; AF031937; AAC12655.1; -
DR EMBL; AF079222; AAD08670.1; -
DR EMBL; AJ005919; CAA06768.1; -
DR EMBL; AJ005920; CAA06768.1; JOINED.
DR EMBL; AJ005921; CAA06768.1; JOINED.
DR EMBL; AJ005922; CAA06768.1; JOINED.
DR EMBL; AJ005923; CAA06768.1; JOINED.
DR EMBL; AJ005924; CAA06768.1; JOINED.
DR EMBL; X64550; CAA45849.1; -
DR EMBL; X64550; CAA45848.1; -
DR MGD; MGI:104667; Hmnr.
KM Hyaluronic acid; Alternative splicing; Repeat; Glycoprotein.
FT DOMAIN 442 546 1.
FT REPEAT 442 546 1.
FT REPEAT 463 483 2.
FT REPEAT 484 504 3.
FT REPEAT 505 525 4.
FT REPEAT 526 546 5.
FT DOMAIN 719 729 5.
FT CARBOHYD 741 750 HYALURONIC ACID-BINDING (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 134 134 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 279 279 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 446 446 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 467 467 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 488 488 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 509 509 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 530 530 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 561 561 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 601 601 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 218 242 MISSING (IN ISOFORM RHAMM1).
FT CONFLICT 19 19 P -> Q (IN REF. 3).
FT CONFLICT 55 55 S -> N (IN REF. 2).
FT CONFLICT 71 71 K -> T (IN REF. 2).
FT CONFLICT 89 91 EKE -> OKH (IN REF. 2).
FT CONFLICT 94 94 A -> V (IN REF. 3).
FT CONFLICT 540 540 S -> T (IN REF. 2).
FT CONFLICT 668 668 E -> D (IN REF. 2).
SQ SEQUENCE 794 AA; 91799 MW; 74DB3D236224499C CRC64;
Query Match 100.0%; Score 54; DB 1; Length 794;
Best Local Similarity 100.0%; Pred. No. 0.019;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 1 KOKIKHVXKL 11
Db 719 KOKIKHVXKL 729
RESULT 4
ID SOK2_YEAST STANDARD; PRT; 785 AA.
AC P53438;
DT 01-OCT-1996 (rel. 34, Created)
DT 01-OCT-1996 (rel. 34, Last sequence update)
DT 01-NOV-1997 (rel. 35, Last annotation update)
DE SOK2 protein.
GN SOK2 OR YMR016C OR YW9711.03C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96069395; PubMed=8524252;
RA Ward M.P., Gimeno C.J., Fink G.R., Garrett S.;
RT "SOK2 may regulate cyclic AMP-dependent protein kinase-stimulated
RT growth and pseudohyphal development by repressing transcription.";
RL Mol. Cell. Biol. 15:6854-6863(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=S288c / AB972;
RA Lye G., Schercher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (May-1995) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: PLAYS A GENERAL REGULATORY ROLE IN THE CYCLIC AMP-
CC DEPENDENT PROTEIN KINASE-STIMULATED (PKA) SIGNAL TRANSDUCTION
CC PATHWAY BY REGULATING THE EXPRESSION OF GENES IMPORTANT IN GROWTH
CC AND DEVELOPMENT. MAY INHIBIT THE SWITCH FROM UNICELLULAR TO
CC FILAMENTOUS GROWTH.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: BELONGS TO THE EFG1/PRD1/STB FAMILY.
CC -----
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CC -----
DR EMBL; S80522; AAB3749.1; -
DR EMBL; 249211; CAA89117.1; -
DR TRANSFAC; T03616; -
DR SGD; S0004618; SOK2.
DR InterPro; IPR003163; Yeast_DNA_bind.
DR Pfam; PF02292; Yeast_DNA_bind; 1.
KM Transcription regulation; Nuclear protein; DNA-binding.
FT DOMAIN 38 45 POLY-GLN.
FT DOMAIN 148 151 POLY-TYR.
FT DOMAIN 169 172 POLY-TYR.
FT DOMAIN 206 217 POLY-GLN.
FT DOMAIN 331 335 POLY-GLN.
FT DOMAIN 526 532 POLY-SER.
SQ SEQUENCE 785 AA; 85643 MW; F4E0F224BB84645F CRC64;
Query Match 66.7%; Score 36; DB 1; Length 785;
Best Local Similarity 66.7%; Pred. No. 40;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
Oy 2 OKIKHVXKL 10
Db 469 EKIRHVXKI 477
RESULT 5
ID RNPA_LACLA STANDARD; PRT; 117 AA.
ID RNPA_LACLA

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AC 09CJ73;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ribonuclease P protein component (EC 3.1.26.5) (RNasep protein) (RNase
DE P protein) (Protein C5).
CN RNP4 OR L10128.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bojoltin A., Wincker P., Mauger S., Jallion O., Malarne K.,
RA Weissenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis IL1403."
RL Genome Res. 11:731-753(2001).
CC -1- FUNCTION: RNasep catalyzes the removal of the 5'-leader sequence
CC from pre-tRNA to produce the mature 5' terminus. It can also
CC cleave other RNA substrates such as 4.5S RNA. The protein
CC component plays an auxiliary but essential role in vivo by binding
CC to the 5'-leader sequence and broadening the substrate specificity
CC of the ribozyme (By similarity).
CC -1- CATALYTIC ACTIVITY: Endonucleolytic cleavage of RNA, removing 5'-
CC extra-nucleotide from tRNA precursor.
CC -1- SUBUNIT: Consists of a catalytic RNA component (M1 or rnpB) and a
CC protein subunit (By similarity).
CC -1- SIMILARITY: BELONGS TO THE RNP4 FAMILY.
CC -----
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CC -----
DR EMBL: AE006251; AFK04226.1; -
DR HSSP: P25814; 1A6F.
DR InterPro: IPR000100; Ribonuclease_P.
DR Pfam: PF00825; Ribonuclease_P.1.
DR TIGRFAMs: TIGR00188; rnpA.1.
DR PROSITE: PS00648; RIBONUCLEASE_P.1.
KW Hydrolyase; Nuclease; Endonuclease; tRNA processing; RNA-binding;
KW Complete proteome.
SQ SEQUENCE 117 AA; 13648 MW; 4F1001A7B4C63C96 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 117;
Best Local Similarity 60.0%; Pred. No. 9.5;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOKIKHVYKL 10
DB 98 KKNLKHVYKL 107

RESULT 6
Y450_MYCPN STANDARD; PRT; 237 AA.
ID Y450_MYCPN
AC P75127;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MG450 homolog (K03_orf237).
GN MPV64 OR MP178.
OS Mycoplasma pneumoniae.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2104;
RN 11;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 29342 / M129;

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RX MEDLINE=97105685; PubMed=8948633;
RA Himmlreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
RA Hermann R.;
RT "Complete sequence analysis of the genome of the bacterium Mycoplasma
RT pneumoniae."
RL Nucleic Acids Res. 24:4420-4449(1996).
CC -----
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CC -----
DR EMBL: AE000019; AAB95826.1; -
DR InterPro: IPR003797; DegV.
DR Pfam: PF02645; DUF194; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 237 AA; 26839 MW; 1E6D6F2BA5D1FDFC CRC64;

Query Match 64.8%; Score 35; DB 1; Length 237;
Best Local Similarity 63.6%; Pred. No. 19;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOKIKHVYKL 11
DB 171 KOLLKHSYKL 181

RESULT 7
RMS5_PENUR
ID RMS5_PENUR STANDARD; PRT; 399 AA.
AC P47907;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Mitochondrial ribosomal protein S5.
OS Penicillium utricae.
OG Mitochondrion.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Penicillium.
OX NCBI_TaxID=29844;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=NRRL 2159A;
RX MEDLINE=96070189; PubMed=7592555;
RA Yamamoto H., Naruse A., Ohsaki T., Sekiguchi J.;
RT "Nucleotide sequence and characterization of the large mitochondrial
RT rRNA gene of Penicillium utricae, and its comparison with those of
RT other filamentous fungi."
RL J. Biochem. 117:888-896(1995).
CC -1- FUNCTION: ESSENTIAL FOR MITOCHONDRIAL PROTEIN SYNTHESIS AND
CC REQUIRED FOR THE MATURATION OF SMALL RIBOSOMAL SUBUNITS
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Mitochondrial.
CC -1- SIMILARITY: BELONGS TO THE VAR1 FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL: D14567; BAA03421.1; -
DR Ribosomal protein; Mitochondrion.
KW Ribosomal protein; Mitochondrion.
SQ SEQUENCE 399 AA; 47447 MW; 38A8263B45BB4041 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 399;
Best Local Similarity 54.5%; Pred. No. 32;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

```

OY 1 KOKIKHVYK 11
111:111111
Db 118 KOKLNYLTK 128

RESULT 8

EFGL_CANAL STANDARD: PRT: 552 AA.
ID EFGL_CANAL
AC P43064;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Enhanced filamentous growth protein.
GN EFGL OR EFG.
OS Candida albicans (Yeast).
OC Eukaryota: Fungi: Ascomycota: Saccharomycotina: Saccharomycetes:
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=3476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 10231;
RX MEDLINE=97299875; PubMed=9155024;
RA Stoldt V.R., Sonneborn A., Leuker C.E., Ernst J.F.;
RT "Egfp, an essential regulator of morphogenesis of the human pathogen Candida albicans, is a member of a conserved class of bHLH proteins regulating morphogenetic processes in fungi.";
RL EMO J. 16:1982-1991(1997).
CC -1- FUNCTION: PUTATIVE TRANSCRIPTION FACTOR THAT STIMULATES PSEUDOTHAL MORPHOGENESIS.
CC -1- SUBCELLULAR LOCATION: Nuclear (potential).
CC -1- SIMILARITY: BELONGS TO THE EFGL/PHD1/STUA FAMILY.

CC -----
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CC -----
DR EMBL: Z32687; CAA83640.1; -
DR InterPro: IPR003163; Yeast_DNA_bind.
DR Pfam: PF02292; Yeast_DNA_bind.1.
KW Transcription regulation; Nuclear protein; DNA-binding.
FT DOMAIN 34 37 POLY-GLN.
FT DOMAIN 46 50 POLY-GLN.
FT DOMAIN 83 93 POLY-GLN.
FT DOMAIN 315 326 POLY-ALA.
FT DOMAIN 332 338 POLY-PRO.
FT DOMAIN 438 446 POLY-GLN.
FT DOMAIN 470 473 POLY-GLN.
FT DOMAIN 483 493 POLY-GLN.
FT DOMAIN 496 499 POLY-GLN.
SQ SEQUENCE 552 AA: 59964 MW: F94FD94FC2E06EB7 CRC64;

Query Match 64.8%; Score 35; DB 1; Length 552;
Best Local Similarity 55.6%; Pred. No. 44;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 2 OKIKHVYK 10
111:111111
Db 259 EKVHVYK 267

RESULT 9

CLC7_MOUSE STANDARD: PRT: 803 AA.
ID CLC7_MOUSE
AC 070496;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 7 (CLC-7).

GN CLCN7 OR CLC7.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21124827; PubMed=11207362;
RA Kornak U., Kasper D., Bosl M.R., Kaiser E., Schweizer M., Schulz A.,
RA Friedrich W., Delling G., Jentsch T.J.;
RT "Loss of the CLC-7 chloride channel leads to osteopetrosis in mice and man.";
RL Cell 104:205-215(2001).

CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME; MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND TRANSEPITHELIAL TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -----
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CC -----

DR EMBL: AF063101; AAC18832.1; -
DR EMBL: AF063098; AAC18832.1; JOINED.
DR EMBL: AF063100; AAC18832.1; JOINED.
DR MGD: MGI:1347048; CLCN7.
DR InterPro: IPR006447; CBS_domain.
DR Pfam: PF00571; CBS; 2.
DR Pfam: PF00654; Voltage_CLC; 1.
DR PRINTS: PR00762; CLCHANNEL.
DR SMART: SM00116; CBS; 2.
KW Ion channel; Ion transport; Voltage-gated channel; Transmembrane; CBS domain; Repeat.
FT TRANSMEM 126 146 POTENTIAL.
FT TRANSMEM 175 195 POTENTIAL.
FT TRANSMEM 222 242 POTENTIAL.
FT TRANSMEM 290 310 POTENTIAL.
FT TRANSMEM 373 393 POTENTIAL.
FT TRANSMEM 410 430 POTENTIAL.
FT TRANSMEM 493 513 POTENTIAL.
FT TRANSMEM 516 536 POTENTIAL.
FT TRANSMEM 579 599 POTENTIAL.
FT TRANSMEM 627 674 CBS 1.
FT DOMAIN 737 781 CBS 2.
SQ SEQUENCE 803 AA: 88712 MW: A7D6DA5791DAA48C CRC64;

Query Match 64.8%; Score 35; DB 1; Length 803;
Best Local Similarity 77.8%; Pred. No. 63;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVYK 11
111:111111
Db 215 KIPHVYK 223

RESULT 10

CLC7_RAT STANDARD: PRT: 803 AA.
ID CLC7_RAT
AC P51799;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 7 (CLC-7).

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OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96130311; PubMed=8543009;
RA Brandt S., Jentsch T.J.;
RT "CLC-6 and CLC-7 are two novel broadly expressed members of the CLC
RT chloride channel family.";
RL FEBS Lett. 377:15-20(1995).
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, TESTIS, MUSCLE AND KIDNEY.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
CC -----
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CC -----
DR EMBL; 267744; CAA91557.1; -.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR001807; CL-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR SMART; SM00116; CBS; 2.
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain; Repeat.
FT TRANSMEM 126 146 POTENTIAL.
FT TRANSMEM 175 195 POTENTIAL.
FT TRANSMEM 222 242 POTENTIAL.
FT TRANSMEM 290 310 POTENTIAL.
FT TRANSMEM 373 393 POTENTIAL.
FT TRANSMEM 410 430 POTENTIAL.
FT TRANSMEM 493 513 POTENTIAL.
FT TRANSMEM 516 536 POTENTIAL.
FT TRANSMEM 579 599 POTENTIAL.
FT TRANSMEM 627 674 CBS 1.
FT DOMAIN 737 781 CBS 2.
SQ SEQUENCE 803 AA; 88730 MW; A7D6AA3D21DA6FED CRC64;

Query Match 64.8%; Score 35; DB 1; Length 803;
Best Local Similarity 77.8%; Pred. NO. 63;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVYKLIK 11
DB 215 KIPHYVRLK 223

RESULT 11
CLC7_HUMAN STANDARD; PRT; 805 AA.
AC P51798; O9NXY5;
DT 01-OCT-1996 (Rel. 34, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Chloride channel protein 7 (CLC-7).
GN CLCN7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;

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RN (1)
RP SEQUENCE FROM N.A.
RA Rae J.L.;
RT "Ion channels in lens epithelia.";
RT Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
RN (2)
RP SEQUENCE FROM N.A.
RC TISSUE=SKIN;
RA Strausberg R.;
RT Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN (3)
RP SEQUENCE OF 17-805 FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=96130311; PubMed=8543009;
RA Brandt S., Jentsch T.J.;
RT "CLC-6 and CLC-7 are two novel broadly expressed members of the CLC
RT chloride channel family.";
RL FEBS Lett. 377:15-20(1995).
RN (4)
RP SEQUENCE OF 275-432 FROM N.A.
RX MEDLINE=98234303; PubMed=9565675;
RA Eggermont J.;
RT "The exon-intron architecture of human chloride channel genes is not
RT conserved.";
RL Blochim. Biophys. Acta 1397:156-160(1998).
RN (5)
RP SEQUENCE OF 744-805 FROM N.A.
RC TISSUE=Breast;
RA Schutte B.C., Malik M.I., Fingert J., Stone E., Lamb F.S.;
RT Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: VOLTAGE-GATED CHLORIDE CHANNEL. CHLORIDE CHANNELS HAVE
CC SEVERAL FUNCTIONS INCLUDING THE REGULATION OF CELL VOLUME;
CC MEMBRANE POTENTIAL STABILIZATION, SIGNAL TRANSDUCTION AND
CC TRANSEPITHELIAL TRANSPORT.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: BRAIN, TESTIS, MUSCLE AND KIDNEY.
CC -1- SIMILARITY: BELONGS TO THE CHLORIDE CHANNEL FAMILY.
CC -1- SIMILARITY: CONTAINS 2 CBS DOMAINS.
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CC -----
DR EMBL; AF224741; AAF34711.1; -.
DR EMBL; BC012737; AAH12737.1; -.
DR EMBL; 267743; CAA91556.1; -.
DR EMBL; AJ001910; CAA05083.1; -.
DR EMBL; U88844; AAB48530.1; -.
DR Genew; HGNC:2025; CLCN7.
DR MIM; 602727; -.
DR InterPro; IPR000644; CBS_domain.
DR InterPro; IPR001807; CL-channel_volt.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF00654; Voltage_CLC; 1.
DR PRINTS; PR00762; CLCHANNEL.
DR SMART; SM00116; CBS; 2.
KW Ionic channel; Ion transport; Voltage-gated channel; Transmembrane;
KW CBS domain; Repeat.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 177 197 POTENTIAL.
FT TRANSMEM 224 244 POTENTIAL.
FT TRANSMEM 292 312 POTENTIAL.
FT TRANSMEM 375 395 POTENTIAL.
FT TRANSMEM 412 432 POTENTIAL.
FT TRANSMEM 495 515 POTENTIAL.
FT TRANSMEM 518 538 POTENTIAL.
FT TRANSMEM 581 601 POTENTIAL.
FT DOMAIN 629 674 CBS 1.
FT DOMAIN 739 783 CBS 2.

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FT CONFLICT 267 267 T -> S (IN REF. 3).
FT CONFLICT 279 279 F -> L (IN REF. 3 AND 4).
SQ SEQUENCE 805 AA; 88679 MW; E56BC04BADE1C695 CRC64;

Query Match
Best Local Similarity 77.8%; Score 35; DB 1; Length 805;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KIKHVKLK 11
   1 1 1 1 1 1
Db 217 KIPHVRLK 225

RESULT 12
MYSN_DROME STANDARD; PRT; 2017 AA.
ID MYSN_DROME
AC 099323;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Myosin heavy chain, non-muscle (zipper protein) (Myosin II).
GN zip.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
OC Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=90349606; PubMed=2117279;
RA Ketchum A.S., Stewart C.T., Stewart M., Kiehart D.P.;
RT "Complete sequence of the Drosophila nonmuscle myosin heavy-chain
transcript: conserved sequences in the myosin tail and differential
splicing in the 5' untranslated sequence."
RL Proc. Natl. Acad. Sci. U.S.A. 87:6316-6320(1990)
CC -1- FUNCTION: NONMUSCLE MYOSIN APPEARS TO BE RESPONSIBLE FOR
CELLULARIZATION. REQUIRED FOR MORPHOGENESIS AND CYTOKINESIS.
CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A
SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.
CC -1- SIMILARITY: CONTAINS 1 MYOSIN-LIKE GLOBULAR HEAD DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IO DOMAIN.
CC
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CC -----
DR EMBL: M35012; AAA28713.1; -
DR PIR: A36014; A36014.
DR PIR: B36014; B36014.
DR HSP: P10587; IBR2.
DR FLYBase: FBgn0005634; zip.
DR InterPro: IPR000048; IO_region.
DR InterPro: IPR004009; Myosin_N.
DR InterPro: IPR002928; Myosin_tail.
DR InterPro: IPR001609; myosin_head.
DR Pfam: PF00063; myosin_head.1.
DR Pfam: PF00612; IO.1.
DR Pfam: PF01576; Myosin_tail.1.
DR Pfam: PF02736; Myosin_N.1.
DR PRINTS: PRO0193; MYOSINHEAVY.
DR PRODOM: PD000355; myosin_head.1.
DR SMART: SMO0015; IO.1.
DR SMART: SMO0242; MYSC.1.
DR PROSITE: PSS0096; IO.1.
DR Myosin: Alternative splicing; Coiled coil; Actin-binding;
KW ATP-binding; Calmodulin-binding.
FT DOMAIN 1 829 MYOSIN HEAD-LIKE.
FT DOMAIN 830 859 IO.

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FT DOMAIN 886 2017 COILED COIL (POTENTIAL).
FT NP_BIND 225 232 ATP.
FT DOMAIN 250 260 25 KDA/50 KDA JUNCTION.
FT DOMAIN 682 694 50 KDA/20 KDA JUNCTION.
FT DOMAIN 705 727 ACTIN-BINDING.
FT DOMAIN 742 758 REACTIVE SULFHYDRYL/ACTIN-BINDING.
FT DOMAIN 1303 2017 LIGHT-MEROMYOSIN (LMW).
FT DOMAIN 1303 1970 ALPHA-HELICAL TAILPIECE (LMW).
FT DOMAIN 1971 2017 GLOBULAR TAILPIECE.
FT VARSPIC 1 45 MISSING (IN SHORT ISOFORM).
SQ SEQUENCE 2017 AA; 232016 MW; 73E3CB02BA8F2528 CRC64;

Query Match
Best Local Similarity 64.8%; Score 35; DB 1; Length 2017;
Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOKHVKLK 11
   : 1 1 1 1 1 1
Db 1063 EERAKHLAKL 1073

RESULT 13
RPL1_PLAFA STANDARD; PRT; 2339 AA.
ID RPL1_PLAFA
AC P27625;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE DNA-directed RNA polymerase III largest subunit (EC 2.7.7.6).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92018020; PubMed=1656254;
RA Li W.B., Bzik D.J., Tanaka M., Gu H., Fox B.A., Inselburg J.;
RT "Characterization of the gene encoding the largest subunit of
Plasmodium falciparum RNA polymerase III."
RL Mol. Biochem. Parasitol. 46:229-240(1991).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
{RNA}(N).
CC -1- SUBUNIT: RNA POLYMERASE III CONSISTS OF ABOUT 15 DIFFERENT
SUBUNITS. THIS SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE
III.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- MISCELLANEOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE
FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA
PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE
III FOR 5S AND TRNA GENES.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC
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CC -----
DR EMBL: M73770; AAA29729.1; -
DR InterPro: IPR000722; RNA_pol_A.
DR InterPro: IPR002879; RNA_pol_A2.
DR Pfam: PF00623; RNA_pol_A.1.
DR Pfam: PF01854; RNA_pol_A2.2.
DR Transferase: DNA-directed RNA polymerase; Transcription; Zinc;
KW Zinc-finger; Nuclear protein.
FT ZN_FING 88 101 C3H-TYPE (POTENTIAL).
SQ SEQUENCE 2339 AA; 272829 MW; EDD899263086FD48 CRC64;

Query Match
64.8%; Score 35; DB 1; Length 2339;

```

Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

OY 3 KIKHVVKL 11
1:1:1:1:1
Db 198 KIKHVVKL 206

RESULT 14

RE1_HUMAN STANDARD: PRT: 196 AA.

ID RE1_HUMAN 095322;
AC 015258; 095322;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE RE1 protein.
GN RE1.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE-Breast cancer;
RX MEDLINE=97454982; PubMed=9109388;
RA Fuellekrug J., Boehm J., Koeltger S., Nilsson T., Mieskes G.,
RA Schmitt H.;

RT "Human Re1 is localized to the Golgi apparatus and complements the
RT deletion of the homologous Re1 protein of Saccharomyces
RT cerevisiae."
RL Eur. J. Cell Biol. 74:31-40(1997).

RN (2)
RP SEQUENCE FROM N.A.

RA Barrow I. K.-P., Boguski M.S., Touchman J., Spencer F.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.

CC -1- FUNCTION: INVOLVED IN THE RETRIEVAL OF ENDOPLASMIC RETICULUM
CC MEMBRANE PROTEINS FROM THE EARLY GOLGI COMPARTMENT (BY
CC SIMILARITY).

CC -1- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. GOLGI.
CC -1- SIMILARITY: BELONGS TO THE RE1 FAMILY.

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CC -----
CC DR EMBL: AJ001421; CA004754.1; -
CC DR EMBL: AF091071; AAC72940.1; -
CC DR InterPro: IPR004932; Re1.
CC DR Pfam: PF03248; Re1; 1.
CC KM Transmembrane: Golgi stack.

FT TRANSMEM 41 61
FT TRANSMEM 63 83
FT TRANSMEM 140 160
FT CONFLICT 123 196

FT TRANSMEM 41 61 POTENTIAL.
FT TRANSMEM 63 83 POTENTIAL.
FT TRANSMEM 140 160 POTENTIAL.
FT CONFLICT 123 196 HAATGILVAVWCTFPDAFVNPVFWPILVVFIMLCITMK
ROIKHMIKRYIPTTHGKRKRRKEDGAKFAS -> DASV
CGDGRCSKAGGCGROCVLAADALTFSPHKACGCGHPC
CYCLYFLRRRQRPVGLDSDVLAHALLYHDEEANOQHD
(IN REF. 2).

FT SEQUENCE 196 AA; 22958 MW; 0FF7F3CDC9F8BA69 CRC64;

Query Match 63.0%; Score 34; DB 1; Length 196;
Best Local Similarity 45.5%; Pred. No. 24;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOKIKHVVKL 11
1:1:1:1:1
Db 163 KOKIKHVVKL 173

RESULT 15
MTM4_METUA STANDARD: PRT: 298 AA.

ID MTM4_METUA 058724;
AC 058724;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Putative modification methylase MjaIVP (EC 2.1.1.-) (M.MjaIVP).
GN MjaIVP OR MJ1328.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC Methanocaldococcaceae; Methanocaldococcus.

OX NCBI_TaxID=2190;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=6688087;

RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Nguyen D.,
RA Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA Uitterlinden T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT jannaschii."
RL Science 273:1058-1073(1996).
CC -1- FUNCTION: THIS METHYLASE RECOGNIZES THE DOUBLE-STRANDED SEQUENCE
CC GTNNAC, CAUSES SPECIFIC METHYLATION ON ? ON BOTH STRANDS, AND
CC PROTECTS THE DNA FROM CLEAVAGE BY THE MJAIV ENDONUCLEASE
CC (POTENTIAL).

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CC -----
CC DR EMBL: U67573; AAB99337.1; -
CC DR REBASE: 3895; M.MjaIVP.
CC DR TIGR: MJ1328; -

CC KM Hypothetical protein: Transferase: Methyltransferase;
CC Restriction system: Complete proteome.
CC SEQUENCE 298 AA; 35328 MW; 9BE52F35B001822B CRC64;

Query Match 63.0%; Score 34; DB 1; Length 298;
Best Local Similarity 66.7%; Pred. No. 37;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOKIKHVVK 9
1:1:1:1:1
Db 241 KOKIKHVVK 249

Search completed: February 8, 2003, 10:41:27
Job time : 8.96667 secs

DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Receptor for hyaluronic acid mediated motility (Fragment).
 GN RHAMM.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=OVARY;
 RA Schoenfelder M., Einspanier R.;
 RT "Expression of HAS-system during oocyte maturation in the cow";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ439694; CAD29126.1; -.
 FT NON_TER 1
 FT 82
 SQ SEQUENCE 82 AA; 9452 MW; 46B87555C0F1B66 CRC64;

Query Match 100.0%; Score 54; DB 6; Length 82;
 Best Local Similarity 100.0%; Pred. No. 0.019;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOKIGHVVKL 11
 Db 28 KOKIGHVVKL 38

RESULT 3
 ID Q92026 PRELIMINARY; PRT; 476 AA.
 AC Q92026;
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Hyaluronan receptor.
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92299690; PubMed=1376732;
 RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D.,
 RA Criggs V., Austen L., Nance D.M., Turley E.A.;
 RT "Molecular cloning of a novel hyaluronan receptor that mediates tumor
 cell motility.";
 RL J. Cell Biol. 117:1343-1350(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92348516; PubMed=1639856;
 RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D.,
 RA Criggs V., Austen L., Nance D.M., Turley E.A.;
 RT "Correction. Molecular cloning of a novel hyaluronan receptor that
 mediates tumor cell motility.";
 RL J. Cell Biol. 118:753-753(1992).
 DR EMBL; S41029; AAA09809.1; -.
 KW Receptor.
 SQ SEQUENCE 476 AA; 55486 MW; 62DCA82045E0CB2 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 476;
 Best Local Similarity 100.0%; Pred. No. 0.094;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOKIGHVVKL 11
 Db 401 KOKIGHVVKL 411

RESULT 4
 Q9WUF7

ID Q9WUF7 PRELIMINARY; PRT; 713 AA.
 AC Q9WUF7;
 DT 01-NOV-1999 (TReMBLrel. 12, Created)
 DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE Hyaluronan receptor RHAMM.
 GN RHAMM.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SPRAGUE DAWLEY;
 RA Li X., Lynn B., Nagy J.I., Cattini P.A.;
 RT "RHAMM cDNA from rat brain.";
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PHOCHROMOCYTOMA;
 RA Lynn B.D., Li X., Cattini P.A., Nagy J.I.;
 RT "Sequence, protein expression and erk association of the hyaladerin
 RHAMM in PC12 cells.";
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF133057; AAU24473.1; -.
 DR EMBL; AF336825; AAK21904.1; -.
 KW Receptor.
 SQ SEQUENCE 713 AA; 82395 MW; 2FE310D5759C6CB3 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 713;
 Best Local Similarity 100.0%; Pred. No. 0.14;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOKIGHVVKL 11
 Db 635 KOKIGHVVKL 645

RESULT 5
 ID Q8VDR2 PRELIMINARY; PRT; 836 AA.
 AC Q8VDR2;
 DT 01-MAR-2002 (TReMBLrel. 20, Created)
 DT 01-MAR-2002 (TReMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Similar to hyaluronan mediated motility receptor (RHAMM).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strauberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021427; AAH21427.1; -.
 KW Receptor.
 SQ SEQUENCE 836 AA; 96670 MW; B9BDDA22BECAC652 CRC64;

Query Match 100.0%; Score 54; DB 11; Length 836;
 Best Local Similarity 100.0%; Pred. No. 0.16;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOKIGHVVKL 11
 Db 761 KOKIGHVVKL 771

RESULT 6
 ID Q9FHM8 PRELIMINARY; PRT; 680 AA.
 AC Q9FHM8;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)

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DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Receptor-like protein kinase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=20181125; PubMed=10718197;
RA Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. X. Sequence
RT features of the regions of 3,076,755 bp covered by sixty P1 and TAC
RT clones."
RL DNA Res. 7:31-63 (2000).
DR EMBL, AB018109; BAB08672.1; -
DR InterPro; IPR000719; Euk_pkinase.
DR InterPro; IPR001611; LRR.
DR InterPro; IPR003592; LRR_out.
DR InterPro; IPR002290; Ser_thr_pkinase.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00560; LRR; 6.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00019; LEURICRPT.
DR ProDom; PD000001; Euk_pkinase; 1.
DR SMART; SM00230; S_TKc; 1.
DR SMART; SM00219; TyKc; 1.
DR SMART; SM00219; TyKc; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR ATP-binding; Kinase; Transferase.
SQ SEQUENCE 680 AA; 74751 MW; D1079C3CF316D36D CRC64;

Query Match 77.8%; Score 42; DB 10; Length 680;
Best Local Similarity 70.0%; Pred. No. 19;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOKIKHVYKL 10
Db 612 KOKYHLYKL 621

RESULT 7
Q8S8K9 PRELIMINARY; PRT; 355 AA.
AC Q8S8K9;
DT 01-JUN-2002 (Tremblrel. 21, Created)
DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Expressed protein.
GN ATG06005.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eucosids II; Brassicales; Brassicaceae; Arabidopsis.
CX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.V. COLUMBIA;
RX Lin X.;
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C.V. COLUMBIA;
RX Town C.D., Kaul S.;
RT Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

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DR EMBL, AC005970; AAM15099.1; -
SQ SEQUENCE 355 AA; 40585 MW; 92EB836EBE367AA2 CRC64;

Query Match 72.2%; Score 39; DB 10; Length 355;
Best Local Similarity 77.8%; Pred. No. 37;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QKIKHVYKL 10
Db 108 QKIKHVYRL 116

RESULT 8
P93142 PRELIMINARY; PRT; 371 AA.
AC P93142;
DT 01-MAY-1997 (Tremblrel. 03, Created)
DT 01-MAY-1997 (Tremblrel. 03, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Dihydroflavonol reductase.
GN DFR.
OS Forsythia intermedia (Border forsythia).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Assteridae; euasterids I; Lamiales; Oleaceae; Forsythia.
CX NCBI_TaxID=55183;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C.V. SPRING GLORY; TISSUE=PETAL;
RX MEDLINE=98009967; PubMed=9349254;
RA Rosati C., Cadic A., Duron M., Renou J.P., Simoneau P.;
RT "Molecular cloning and expression analysis of dihydroflavonol 4-
RT reductase gene in flower organs of Forsythia x intermedia."
RT Plant Mol. Biol. 35:303-311 (1997).
RL EMBL, Y09127; CAA70345.1; -
SQ SEQUENCE 371 AA; 41856 MW; 4PAF14F5FA8B366 CRC64;

Query Match 70.4%; Score 38; DB 10; Length 371;
Best Local Similarity 60.0%; Pred. No. 58;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KOKIKHVYKL 10
Db 47 KOKYHLYKL 56

RESULT 9
Q9AVX8 PRELIMINARY; PRT; 861 AA.
AC Q9AVX8;
DT 01-JUN-2001 (Tremblrel. 17, Created)
DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Hypothetical 104.0 kDa protein.
OS Guillardia theta (Cryptomonas phi).
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
CX NCBI_TaxID=55529;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087226; PubMed=10618395;
RA Zauner S., Fraunholz M., Wastl J., Penny S.L., Beaton M.,
RA Cavalier-Smith T., Maier U., Douglas S.;
RT "Chloroplast protein and centromal genes, a tRNA intron, and odd
RT telomeres in an unusually compact eukaryotic genome, the cryptomonad
RT nucleomorph."
RL Proc. Natl. Acad. Sci. U.S.A. 97:200-205 (2000).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21223349; PubMed=11333671;
RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.,
RA Wu X., Reich M., Cavalier-Smith T., Maier U.;
RT "The highly reduced genome of an enslaved algal nucleus."
RT Nature 410:1091-1096 (2001).

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DR EMBL; AJ010592; CAC27093.1; -.
KW Hypothetical protein.
SQ SEQUENCE 861 AA; 104022 MW; 19DCF355FB47CEC2 CRC64;

Query Match
Best Local Similarity 70.4%; Score 38; DB 10; Length 861;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 K0KIKHVVKLK 11
| | | | |
Db 212 K0KIKHVVKLK 222

RESULT 10
O9LEU2 PRELIMINARY; PRT; 148 AA.
O9LEU2:
AC 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Hypothetical 16.9 kDa protein.
GN T30N20.260.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eustoids 11; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Berman M., Peters S.A., van Staveren M., Dirkse W., Stiekema W.,
RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Meyer K.F.X.;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL365234; CAB96854.1; -.
DR InterPro; IPR003676; Auxin_inducible.
DR Pfam; PF02519; Auxin_inducible; 1.
KW Hypothetical protein.
SQ SEQUENCE 148 AA; 16863 MW; B576A5C89905AB12 CRC64;

Query Match
Best Local Similarity 68.5%; Score 37; DB 10; Length 148;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Oy 3 KIKHVVKLK 11
| | | | |
Db 10 KIKHVVKLK 18

RESULT 11
O9VBU6 PRELIMINARY; PRT; 203 AA.
O9VBU6:
AC 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE CG11857 protein (RE24638p).
GN CG11857.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=BERKELEY;
RC MEDLINE=20196006; PubMed=10731132;
RX Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.P.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

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RA Brandon R.C., Rogers Y.-H.C., Blazew R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
RA Butts J.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke S., Davenport L.B., Davies P.,
RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Honck J.,
RA Hooten D., Houston K.A., Howland T.J., Wei M.-H., Ibeagwan C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclab J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
RA Williams S.W., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RL "The genome sequence of Drosophila melanogaster."
RT SEQUENCE 287:2185-2195(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fiske E.,
RA George R., Gonzalez M., Guarin H., Kronmiller B., Li P., Liao G.,
RA Miranda A., Mungall C.J., Nunco J., Paclab J., Paragas V., Park S.,
RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA Celinker S.;
RL Submitted (APR-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; AE003751; AAF56431.1; -.
DR EMBL; AY094863; AAM11216.1; -.
DR FlyBase; FBgn0039303; CG11857.
DR InterPro; IPR004932; Ret1.
DR Pfam; PF03248; Ret1; 1.
SQ SEQUENCE 203 AA; 23721 MW; 866928F44B443D8 CRC64;

Query Match
Best Local Similarity 54.5%; Score 37; DB 5; Length 203;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy 1 K0KIKHVVKLK 11
| | | | |
Db 163 K0KIKHVVKLK 173

RESULT 12
O99QZ8 PRELIMINARY; PRT; 624 AA.
O99QZ8:
AC 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Hypothetical protein SAV2640.
GN SAV2640 OR SA2433.
OS Staphylococcus aureus (strain Mu50 / ATCC 700699), and
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.

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OX NCBI_TaxID=158878, 158879;
RN
  [1]
  RP SEQUENCE FROM N.A.
  RC SPECIES=S.aureus (strain Mu50), and S.aureus (strain N315);
  RX MEDLINE=21311952; PubMed=11418146;
  RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
  RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Itan J.-O., Ito T.,
  RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,
  RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
  RA Sekizumi K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
  RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
  RA Hattori M., Ogasawara N., Hayashi H., Hiratsuki K.;
  RT "Whole genome sequencing of methicillin-resistant Staphylococcus
  RT aureus.";
  RL Lancet 357:1225-1240(2001).
  DR EMBL; AP003366; BAB58802.1; -.
  DR EMBL; AP003368; BAB43738.1; -.
  DR InterPro; IPR001550; BglG_antitermin.
  DR InterPro; IPR002178; PTS_EIIA_2.
  DR Pfam; PF00874; BglG_antitermin; 1.
  DR Pfam; PF00359; PTS_EIIA_2; 1.
  DR ProDom; PD001689; PTS_EIIA_2; 1.
  DR PROSITE; PS00372; PTS_EIIA_2; UNKNOWN_1.
  KM Hypothetical protein; Complete proteome.
  SQ SEQUENCE 624 AA; 72964 MW; 06476A5EA0DAA2C7 CRC64;

Query Match      68.5%; Score 37; DB 16; Length 624;
Best Local Similarity 63.6%; Pred. No. 1.4e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KOKIKHYVVK 11
Db 464 RHKIRHYVVK 474

RESULT 13
Q9AVW8 PRELIMINARY; PRT; 1473 AA.
AC Q9AVW8;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE DNA-directed RNA polymerase II largest chain (EC 2.7.7.6).
GN RPB1.
OS Guillardia theta (Cryptomonas phi).
OC Eukaryota; Cryptophyta; Cryptomonadaceae; Guillardia.
OX NCBI_TaxID=55529;
RN
  [1]
  RP SEQUENCE FROM N.A.
  RX MEDLINE=20087226; PubMed=10618395;
  RA Zauner S., Fraunholz M., Wasel U., Penny S.L., Beaton M.,
  RA Cavalier-Smith T., Maier U., Douglas S.;
  RT "Chloroplast protein and centosomal genes, a tRNA intron, and odd
  RT telomeres in an unusually compact eukaryotic genome, the cryptomonad
  RT nucleomorph.";
  RL Proc. Natl. Acad. Sci. U.S.A. 97:200-205(2000).
  RN
  [2]
  RP SEQUENCE FROM N.A.
  RX MEDLINE=21223349; PubMed=11323671;
  RA Douglas S., Zauner S., Fraunholz M., Beaton M., Penny S., Deng L.,
  RA Wu X., Reith M., Cavalier-Smith T., Maier U.;
  RT "The highly reduced genome of an enslaved algal nucleus.";
  RL Nature 410:1091-1096(2001).
  DR EMBL; AJ010592; CAC27103.1; -.
  DR InterPro; IPR000722; RNA_pol_A.
  DR InterPro; IPR002879; RNA_pol_A2.
  DR Pfam; PF00623; RNA_pol_A; 1.
  DR Pfam; PF01854; RNA_pol_A2; 1.
  KM DNA-directed RNA polymerase; Nucleotidyltransferase; Transferase.
  SQ SEQUENCE 1473 AA; 168897 MW; FA556B4C96F0BFD CRC64;

Query Match      68.5%; Score 37; DB 10; Length 1473;
Best Local Similarity 70.0%; Pred. No. 3.1e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 QKIKHYVVK 11
Db 112 QKIKHYVVK 121

RESULT 14
Q9LZAB PRELIMINARY; PRT; 1495 AA.
AC Q9LZAB;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical 169.3 kDa protein.
GN P8F6_230.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN
  [1]
  RP SEQUENCE FROM N.A.
  RA Bevan M., Peters S.A., van Staveren M., Dirks W., Stiekema W.,
  RA Bancroft I., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
  RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
  RN
  [2]
  RP SEQUENCE FROM N.A.
  RA Arabidopsis sequencing project;
  RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
  DR EMBL; AL162873; CAB85522.1; -.
  KM Hypothetical protein.
  SQ SEQUENCE 1495 AA; 169293 MW; B5F24EAP952E5AE CRC64;

Query Match      68.5%; Score 37; DB 10; Length 1495;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KOKIKHYVVK 9
Db 584 KKKYKHYVVK 592

RESULT 15
Q8XHUS PRELIMINARY; PRT; 102 AA.
AC Q8XHUS;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein CPE2382.
GN CPE2382.
OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN
  [1]
  RP SEQUENCE FROM N.A.
  RC STRAIN=13 / TYPE A;
  RX PubMed=11792842;
  RA Shimizu T., Ohtani K., Hirakawa H., Oshima K., Yamashita A.,
  RA Shiba T., Ogasawara N., Hattori M., Kuhara S., Hayashi H.;
  RT "Complete genome sequence of Clostridium perfringens, an anaerobic
  RT flesh-eater.";
  RL Proc. Natl. Acad. Sci. U.S.A. 99:996-1001(2002).
  DR EMBL; AP003194; BAB82088.1; -.
  KM Hypothetical protein; Complete proteome.
  SQ SEQUENCE 102 AA; 11428 MW; 53E653C459A0CB7 CRC64;

Query Match      66.7%; Score 36; DB 16; Length 102;
Best Local Similarity 87.5%; Pred. No. 41;
Matches 7; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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OY 1 KOKIGHV 8
:|||||
Db 58 KKKIGHV 65

Search completed: February 8, 2003, 10:42:43
Job time : 27.9333 secs

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GenCore version 5.1.3
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OW protein - protein search, using sw model

Run on: February 8, 2003, 10:42:50 ; Search time 7.7 Seconds
(without alignments)
31.670 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KOKIKHYVKLK 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008

Listing first 45 summaries

Database : Published Applications_AA:*
1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep:*
11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	12	US-08-996-470-1	Sequence 1, Appli
2	36	66.7	785	US-09-801-368-348	Sequence 348, App
3	34	63.0	30	US-09-864-761-34027	Sequence 34027, A
4	34	63.0	196	US-09-840-787-35	Sequence 35, Appl
5	34	63.0	237	US-09-799-777-73	Sequence 73, Appl
6	34	63.0	481	US-09-815-242-11507	Sequence 11507, A
7	34	63.0	747	US-09-974-143A-2	Sequence 2, Appli
8	34	63.0	747	US-09-431-226-7	Sequence 7, Appli
9	33	61.1	108	US-09-815-242-10790	Sequence 10790, A
10	33	61.1	330	US-09-870-759-82	Sequence 82, Appl
11	33	61.1	809	US-10-105-695-2	Sequence 2, Appli
12	33	61.1	809	US-09-747-521-2	Sequence 2, Appli
13	33	61.1	809	US-10-106-014-2	Sequence 2, Appli
14	33	61.1	809	US-09-930-871-8	Sequence 8, Appli
15	33	61.1	1387	US-09-930-871-10	Sequence 10, Appl
16	33	61.1	1392	US-09-930-871-18	Sequence 18, Appl
17	33	61.1	1398	US-09-930-871-20	Sequence 20, Appl
18	33	61.1	1442	US-09-930-871-6	Sequence 6, Appli
19	33	61.1	1442	US-09-930-871-6	Sequence 6, Appli

20	33	61.1	1453	US-09-930-871-16	Sequence 16, Appl
21	33	61.1	1962	US-09-930-871-4	Sequence 4, Appl1
22	33	61.1	1973	US-09-930-871-14	Sequence 14, Appl
23	33	61.1	1998	US-09-930-871-2	Sequence 2, Appl1
24	33	61.1	2009	US-09-930-871-12	Sequence 12, Appl
25	32	59.3	39	US-09-864-761-46628	Sequence 46628, A
26	32	59.3	131	US-09-788-626-4317	Sequence 4317, Ap
27	32	59.3	213	US-09-881-752A-370	Sequence 370, App
28	32	59.3	281	US-09-895-913A-282	Sequence 282, App
29	32	59.3	281	US-09-853-701-17	Sequence 17, Appl
30	32	59.3	400	US-09-815-242-5324	Sequence 5324, Ap
31	31.5	58.3	125	US-09-925-301-933	Sequence 933, App
32	31.5	58.3	359	US-09-799-777-45	Sequence 45, Appl
33	31	57.4	67	US-09-925-299-1310	Sequence 1310, Ap
34	31	57.4	132	US-10-003-035-43	Sequence 43, Appl
35	31	57.4	179	US-10-003-035-44	Sequence 44, Appl
36	31	57.4	179	US-09-872-523-59	Sequence 59, Appl
37	31	57.4	186	US-10-003-035-45	Sequence 45, Appl
38	31	57.4	237	US-09-815-242-5666	Sequence 5666, Ap
39	31	57.4	258	US-09-815-242-12207	Sequence 12207, A
40	31	57.4	295	US-09-510-332-143	Sequence 143, App
41	31	57.4	335	US-10-076-785-12	Sequence 12, Appl
42	31	57.4	338	US-10-076-785-10	Sequence 10, Appl
43	31	57.4	363	US-10-003-035-37	Sequence 37, Appl
44	31	57.4	363	US-09-943-722-130	Sequence 130, App
45	31	57.4	368	US-09-925-299-888	Sequence 888, App

ALIGNMENTS

RESULT 1
US-08-996-470-1
Sequence 1, Application US/08996470A
Patent No. US2002007314A1
GENERAL INFORMATION:
APPLICANT: FAIR
TITLE OF INVENTION: Use of Hyaluronic Acid and Forms to Prevent Arterial
DISEASE
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/08/996,470A
CURRENT FILING DATE: 1997-12-22
EARLIER APPLICATION NUMBER: US 07/675,908
EARLIER FILING DATE: 1991-07-03
EARLIER APPLICATION NUMBER: US 07/838,674
EARLIER FILING DATE: 1992-02-21
EARLIER APPLICATION NUMBER: US 07/838,675
EARLIER FILING DATE: 1992-02-21
EARLIER APPLICATION NUMBER: US 08/125,398
EARLIER FILING DATE: 1993-09-23
EARLIER APPLICATION NUMBER: US 08/285,764
EARLIER FILING DATE: 1994-08-03
EARLIER APPLICATION NUMBER: US 07/952,095
EARLIER FILING DATE: 1992-09-28
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: BINDING
LOCATION: (1)..(12)
OTHER INFORMATION: A peptide mimicking Domain I (amino acids 401-411)
of the hyaluronic acid binding region of RHAMM
US-08-996-470-1

Query Match 100.0%; Score 54; DB 8; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.001;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 KOKIKHYVKLK 11
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Db 2 K0K1KHVVKL 12

RESULT 2

US-09-801-368-348

Sequence 348, Application US/09801368

Patent No. US20020128250A1

GENERAL INFORMATION:

APPLICANT: Busby, Robert

APPLICANT: Call, Brian

APPLICANT: Hecht, Peter

APPLICANT: Holtzman, Doug

APPLICANT: Madden, Kevin

APPLICANT: Maxon, Mary

APPLICANT: Milne, Todd

APPLICANT: No. US20020128250A1man, Thea

APPLICANT: Royer, John

APPLICANT: Salama, Sofie

APPLICANT: Sherman, Amlr

APPLICANT: Silva, Jelf

APPLICANT: Summers, Eric

TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi

FILE REFERENCE: 109272.147

CURRENT APPLICATION NUMBER: US/09/801,368

PRIOR FILING DATE: 2001-03-07

PRIOR APPLICATION NUMBER: US 09/487,558

PRIOR FILING DATE: 2000-01-19

PRIOR APPLICATION NUMBER: US 60/160,587

PRIOR FILING DATE: 1999-10-20

NUMBER OF SEQ ID NOS: 440

SOFTWARE: Patent version 3.0

SEQ ID NO 348

LENGTH: 785

TYPE: PRT

ORGANISM: Saccharomyces cerevisiae

US-09-801-368-348

Query Match 66.7%; Score 36; DB 10; Length 785;

Best Local Similarity 66.7%; Pred. No. 80;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 2 0K1KHVVKL 10

Db 469 EK1RHVKI 477

RESULT 3

US-09-864-761-34027

Sequence 34027, Application US/09864761

Patent No. US20020048763A1

GENERAL INFORMATION:

APPLICANT: Penn, Sharron G.

APPLICANT: Rank, David R.

APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wensheng

TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

FILE REFERENCE: Aeomica-X-1

CURRENT APPLICATION NUMBER: US/09/864,761

PRIOR FILING DATE: 2001-05-23

PRIOR APPLICATION NUMBER: US 60/180,312

PRIOR FILING DATE: 2000-02-04

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 09/632,366

PRIOR FILING DATE: 2000-08-03

PRIOR APPLICATION NUMBER: GB 24263.6

PRIOR FILING DATE: 2000-10-04

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

PRIOR APPLICATION NUMBER: PCT/US01/00666

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00667

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00664

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00665

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00668

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00663

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00662

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00670

PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: US 60/234,687

PRIOR FILING DATE: 2000-09-21

PRIOR APPLICATION NUMBER: US 09/608,408

PRIOR FILING DATE: 2000-06-30

PRIOR APPLICATION NUMBER: US 09/774,203

PRIOR FILING DATE: 2001-01-29

NUMBER OF SEQ ID NOS: 49117

SOFTWARE: Anomax Sequence Listing Engine vers. 1.1

SEQ ID NO 34027

LENGTH: 30

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: MAP TO AC005060.2

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.2

OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 2.8

OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 3

OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5

OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.3

OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.7

OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4

OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 3

OTHER INFORMATION: SWISSPROT HIT: P21439, EVALUE 1.10e-01

US-09-864-761-34027

Query Match 63.0%; Score 34; DB 10; Length 30;

Best Local Similarity 54.5%; Pred. No. 6.1;

Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 K0K1KHVVKL 11

Db 20 K0ELKHGKVK 30

RESULT 4

US-09-840-787-35

Sequence 35, Application US/09840787

Patent No. US20020058264A1

GENERAL INFORMATION:

APPLICANT: Lal, Preeti

APPLICANT: Hillman, Jennifer L.

APPLICANT: Bandman, Olga

APPLICANT: Shah, Purvi

APPLICANT: Au-Young, Janice

APPLICANT: Yue, Henry

APPLICANT: Guegler, Karl J.

APPLICANT: Corley, Neil C.

TITLE OF INVENTION: HUMAN REGULATORY MOLECULES

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESS: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/840,787
FILING DATE: 23-Apr-2001
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/518,865
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 196 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: BLADNOT06
CLONE: 1720770
SEQUENCE DESCRIPTION: SEQ ID NO: 35 :
US-09-840-787-35
Query Match 63.0%; Score 34; DB 10; Length 196;
Best Local Similarity 45.5%; Pred. No. 42;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 KOKIKHVYVK 11
1::111::1:
DB 163 KROIKHMIRYR 173
RESULT 5
US-09-799-777-73
Sequence 73, Application US/09799777
Patent No. US20020091244A1
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
Hillman, Jennifer L.
Corley, Neil C.
Guegler, Karl J.
Baugh, Mariah
Sather, Susan
Shah, Purvi
TITLE OF INVENTION: HUMAN SIGNAL PEPTIDE-CONTAINING PROTEINS
NUMBER OF SEQUENCES: 154
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/799,777
FILING DATE: 06-Mar-2001
CLASSIFICATION: <unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/002,485
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: BILLINGS, LUCY J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0459 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 237 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LUNGUT13
CLONE: 3115936
SEQUENCE DESCRIPTION: SEQ ID NO: 73 :
US-09-799-777-73
Query Match 63.0%; Score 34; DB 10; Length 237;
Best Local Similarity 45.5%; Pred. No. 51;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 1 KOKIKHVYVK 11
1::111::1:
DB 204 KROIKHMIRYR 214
RESULT 6
US-09-815-242-11507
Sequence 11507, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zyskind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 11507
LENGTH: 481
TYPE: PRT
ORGANISM: Helicobacter pylori
US-09-815-242-11507
Query Match 63.0%; Score 34; DB 10; Length 481;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;

Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 OKIKHVYKL 10
||:|||||
Db 246 OKLKYVVKM 254

RESULT 7
US-09-974-143A-2
; Sequence 2, Application US/09974143A
; Publication No. US2003002326A1
; GENERAL INFORMATION:
; APPLICANT: Nezu, Jun-ichi
; TITLE OF INVENTION: NOVEL FETAL GENES
; FILE REFERENCE: 06501-089001
; CURRENT APPLICATION NUMBER: US/09/974,143A
; PRIOR FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: PCT/JP00/02281
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: JP 11/103356
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-974-143A-2

Query Match 63.0%; Score 34; DB 9; Length 747;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOKIKHVYKL 11
:| | | | | | |
Db 131 EQKEKHVYK 141

RESULT 8
US-09-431-226-7
; Sequence 7, Application US/09431226
; Patent No. US2002011559A1
; GENERAL INFORMATION:
; APPLICANT: VERNOS, Isabelle
; APPLICANT: KARSENTI, Eric
; APPLICANT: WITTMANN, Torsten
; TITLE OF INVENTION: TPX2
; FILE REFERENCE: 100564-09045
; CURRENT APPLICATION NUMBER: US/09/431,226
; CURRENT FILING DATE: 1999-11-01
; PRIOR APPLICATION NUMBER: EP 99106710.9
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-431-226-7

Query Match 63.0%; Score 34; DB 10; Length 747;
Best Local Similarity 63.6%; Pred. No. 1.7e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOKIKHVYKL 11
:| | | | | | |
Db 131 EQKEKHVYK 141

RESULT 9
US-09-815-242-10790
; Sequence 10750, Application US/09815242

; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10790
; LENGTH: 108
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-815-242-10790

Query Match 61.1%; Score 33; DB 10; Length 108;
Best Local Similarity 50.0%; Pred. No. 34;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOKIKHVYKL 10
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Db 12 EEOYKHVYK 21

RESULT 10
US-09-870-759-82
; Sequence 82, Application US/09870759
; Patent No. US2002017551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 82
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-82

Query Match 61.1%; Score 33; DB 9; Length 330;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOKIKHVYK 9
|:|:|:|:|
Db 144 KEKIOHVYK 152

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RESULT 11
US-10-105-695-2
; Sequence 2, Application US/10105695
; Publication No. US20020197272A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis
; FILE REFERENCE: 22727/04115
; CURRENT APPLICATION NUMBER: US/10/105,695
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-105-695-2

Query Match      61.1%; Score 33; DB 9; Length 809;
Best Local Similarity 45.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 KOKIKHVYK 11
       1:|||||:
       70 KEIMKHIVKIE 80

Db

RESULT 12
US-10-105-694-2
; Sequence 2, Application US/10105694
; Publication No. US20030003109A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis
; FILE REFERENCE: 22727/04116
; CURRENT APPLICATION NUMBER: US/10/105,694
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-105-694-2

Query Match      61.1%; Score 33; DB 9; Length 809;
Best Local Similarity 45.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 KOKIKHVYK 11
       1:|||||:
       70 KEIMKHIVKIE 80

Db

RESULT 13
US-09-747-521-2
; Sequence 2, Application US/09747521
; Patent No. US20020051791A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel
; APPLICANT: Mateczun, Alfred
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis
; FILE REFERENCE: 22727/04079
; CURRENT APPLICATION NUMBER: US/09/747,521
; CURRENT FILING DATE: 2000-12-21
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; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-09-747-521-2

Query Match      61.1%; Score 33; DB 10; Length 809;
Best Local Similarity 45.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 KOKIKHVYK 11
       1:|||||:
       70 KEIMKHIVKIE 80

Db

RESULT 14
US-10-106-014-2
; Sequence 2, Application US/10106014
; Patent No. US20020142002A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis
; FILE REFERENCE: 22727/04114
; CURRENT APPLICATION NUMBER: US/10/106,014
; PRIOR FILING DATE: 2002-03-25
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 809
; TYPE: PRT
; ORGANISM: Bacillus anthracis
US-10-106-014-2

Query Match      61.1%; Score 33; DB 12; Length 809;
Best Local Similarity 45.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      1 KOKIKHVYK 11
       1:|||||:
       70 KEIMKHIVKIE 80

Db

RESULT 15
US-09-930-871-8
; Sequence 8, Application US/09930871
; Patent No. US20020076780A1
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Daniel
; TITLE OF INVENTION: No. US20020076780A1 Human Ion Channel Proteins and Polynucleotides
; FILE REFERENCE: LEX-0216-USA
; CURRENT APPLICATION NUMBER: US/09/930,871
; PRIOR FILING DATE: 2001-08-14
; PRIOR FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 1381
; TYPE: PRT
; ORGANISM: homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: (1)...(1381)
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-930-871-8
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Query Match 61.1%; Score 33; DB 10; Length 1381;
Best Local Similarity 75.0%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVKL 10
I:|||||
Db 745 KVKHVNL 752

Search completed: February 8, 2003, 10:52:09
Job time : 8.7 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2003, 10:41:05 ; Search time 146.3 Seconds
(without alignments)
48.476 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KQKKHVKLK 11

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Gapop 10.0 , Gapext 0.5

Searched: 4569144 segs, 64473110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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26: /cgn2_6/ptodata/1/paa/US102_COMB.pep.*
27: /cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	11	7	US-08-318-892-3
2	54	100.0	11	7	US-08-318-892B-3
3	54	100.0	11	15	US-09-169-077-1
4	54	100.0	11	18	US-09-424-292-4
5	54	100.0	11	20	US-09-685-010-30
6	54	100.0	11	23	US-09-978-309A-30

7	54	100.0	12	7	US-08-318-892-9	Sequence 9, Appl1
8	54	100.0	12	7	US-08-318-892B-9	Sequence 9, Appl1
9	54	100.0	12	13	US-08-996-470-1	Sequence 1, Appl1
10	54	100.0	32	20	US-09-685-010-51	Sequence 51, Appl1
11	54	100.0	32	23	US-09-978-309A-51	Sequence 51, Appl1
12	54	100.0	32	23	US-09-978-309A-81	Sequence 81, Appl1
13	54	100.0	32	23	US-09-978-309A-82	Sequence 82, Appl1
14	54	100.0	42	20	US-09-657-276-1174	Sequence 1174, Ap
15	54	100.0	221	23	US-09-978-309A-75	Sequence 75, Appl1
16	54	100.0	221	23	US-09-978-309A-76	Sequence 76, Appl1
17	54	100.0	242	21	US-09-758-470-463	Sequence 463, App
18	54	100.0	242	23	US-09-978-309A-74	Sequence 74, Appl1
19	54	100.0	242	26	US-10-211-818-463	Sequence 463, App
20	54	100.0	333	23	US-09-978-309A-73	Sequence 73, Appl1
21	54	100.0	352	23	US-09-978-309A-83	Sequence 83, Appl1
22	54	100.0	407	23	US-09-978-309A-78	Sequence 78, Appl1
23	54	100.0	428	7	US-08-318-892B-33	Sequence 33, Appl1
24	54	100.0	435	23	US-09-978-309A-80	Sequence 80, Appl1
25	54	100.0	476	7	US-08-318-892-2	Sequence 2, Appl1
26	54	100.0	476	21	US-09-791-537-42360	Sequence 42360, A
27	54	100.0	476	23	US-09-978-309A-77	Sequence 77, Appl1
28	54	100.0	476	23	US-09-978-309A-79	Sequence 79, Appl1
29	54	100.0	477	7	US-08-318-892B-2	Sequence 2, Appl1
30	54	100.0	477	21	US-09-791-537-88053	Sequence 88053, A
31	54	100.0	606	21	US-09-791-537-67341	Sequence 67341, A
32	54	100.0	630	15	US-09-169-077-6	Sequence 6, Appl1
33	54	100.0	631	20	US-09-685-010-48	Sequence 48, Appl1
34	54	100.0	631	23	US-09-978-309A-48	Sequence 48, Appl1
35	54	100.0	646	24	US-10-023-634-16	Sequence 16, Appl1
36	54	100.0	676	26	US-10-256-250-16	Sequence 16, Appl1
37	54	100.0	709	24	US-10-023-634-14	Sequence 14, Appl1
38	54	100.0	709	24	US-10-023-634-18	Sequence 18, Appl1
39	54	100.0	709	24	US-10-023-634-77	Sequence 77, Appl1
40	54	100.0	709	26	US-10-256-250-15	Sequence 15, Appl1
41	54	100.0	713	24	US-10-023-634-81	Sequence 81, Appl1
42	54	100.0	723	24	US-10-023-634-80	Sequence 80, Appl1
43	54	100.0	725	15	US-09-169-077-4	Sequence 4, Appl1
44	54	100.0	725	20	US-09-685-010-47	Sequence 47, Appl1
45	54	100.0	725	23	US-09-978-309A-47	Sequence 47, Appl1

ALIGNMENTS

RESULT 1
US-08-318-892-3
Sequence 3, Application US/08318892
GENERAL INFORMATION:
APPLICANT: Tuttle, Eva A
TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR
TITLE OF INVENTION: FOR HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESS: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,892
FILING DATE: 1-DEC-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pierr1, Margaret A
REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIM-8

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-318-892-3

Query Match          100.0%; Score 54; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KOKIKHVVKLK 11
DB 1 KOKIKHVVKLK 11
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RESULT 2
US-08-318-892B-3
; Sequence 3, Application US/08318892B
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR FOR
; TITLE OF INVENTION: HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING PEPTIDES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,892B
; FILING DATE: 1-DEC-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pierli, Margaret A
; REGISTRATION NUMBER: 30709
; REFERENCE/DOCKET NUMBER: SIM-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-08-318-892B-3

Query Match          100.0%; Score 54; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KOKIKHVVKLK 11
DB 1 KOKIKHVVKLK 11
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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN HYALURONAN RECEPTOR
; NUMBER OF SEQUENCES: 52
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,077
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CA97/00240
; FILING DATE:
; APPLICATION NUMBER: GB 9607441.4
; FILING DATE: 10-APR-1996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
;
US-09-169-077-1

Query Match          100.0%; Score 54; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KOKIKHVVKLK 11
DB 1 KOKIKHVVKLK 11
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RESULT 4
US-09-424-292-4
; Sequence 4, Application US/09424292
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: Improved Delivery of Disease Modifiers
; FILE REFERENCE: 205375
; CURRENT APPLICATION NUMBER: US/09/424,292
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: PCT/CA98/00448
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: CA 2,205,771
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
;
US-09-424-292-4

Query Match          100.0%; Score 54; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KOKIKHVVKLK 11
DB 1 KOKIKHVVKLK 11
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```

RESULT 3
US-09-169-077-1
; Sequence 1, Application US/09169077
; APPLICANT: Cruz, Tony F.
```

```

RESULT 5
US-09-685-010-30
; Sequence 30, Application US/09685010
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A.
; APPLICANT: Cruz, Tony F.
```



```

: TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
: TITLE OF INVENTION: CELLULAR RESPONSE TO INJURY AND OTHER PROLIFERATING CELL
: FILE REFERENCE: 910130.401C1
: CURRENT APPLICATION NUMBER: US/09/685.010
: CURRENT FILING DATE: 2001-05-23
: NUMBER OF SEQ ID NOS: 72
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 30
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Peptide composition that binds a hyalauronan
US-09-685-010-30

Query Match      100.0%; Score 54; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KOKIKHVVKLK 11
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Db      1 KOKIKHVVKLK 11

RESULT 6
US-09-978-309A-30
: Sequence 30, Application US/09978309A
: GENERAL INFORMATION:
: APPLICANT: Cruz, Tony
: APPLICANT: Pastrik, Aleksandra
: APPLICANT: Turley, Eva A.
: TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
: TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
: TITLE OF INVENTION: Hyaladerlin and Hyaluronans
: FILE REFERENCE: 033352-010
: CURRENT APPLICATION NUMBER: US/09/978,309A
: CURRENT FILING DATE: 2002-04-04
: PRIOR APPLICATION NUMBER: US 09/685,010
: PRIOR FILING DATE: 2000-10-05
: PRIOR APPLICATION NUMBER: US 09/541,522
: PRIOR FILING DATE: 2000-04-03
: PRIOR APPLICATION NUMBER: US 60/127,457
: PRIOR FILING DATE: 1999-04-01
: NUMBER OF SEQ ID NOS: 84
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 30
: LENGTH: 11
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Peptide composition that binds a hyalauronan
US-09-978-309A-30

Query Match      100.0%; Score 54; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KOKIKHVVKLK 11
        |||
Db      1 KOKIKHVVKLK 11

RESULT 7
US-08-318-892-9
: Sequence 9, Application US/08318892
: GENERAL INFORMATION:
: APPLICANT: Turley, Eva A
: APPLICANT: Turley, Eva A
: TITLE OF INVENTION: HALURONAN RECEPTOR (RHAM = RECEPTOR
: TITLE OF INVENTION: FOR HALURONAN MEDIATED MOBILITY) AND HALURONAN BINDING
: TITLE OF INVENTION: PEPTIDES
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
```

```

: ADDRESSEE: C/O FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: N.Y.
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: WordPerfect 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/318,892
: FILING DATE: 1-DEC-1994
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Pierri, Margaret A
: REGISTRATION NUMBER: 30,709
: REFERENCE/DOCKET NUMBER: STM-8
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 12 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
US-08-318-892-9

Query Match      100.0%; Score 54; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KOKIKHVVKLK 11
        |||
Db      2 KOKIKHVVKLK 12

RESULT 8
US-08-318-892B-9
: Sequence 9, Application US/08318892B
: GENERAL INFORMATION:
: APPLICANT: Turley, Eva A
: APPLICANT: Turley, Eva A
: TITLE OF INVENTION: HALURONAN RECEPTOR (RHAM = RECEPTOR FOR
: TITLE OF INVENTION: HALURONAN MEDIATED MOBILITY) AND HALURONAN BINDING PEPTID
: NUMBER OF SEQUENCES: 41
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: C/O FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: N.Y.
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/318,892B
: FILING DATE: 1-DEC-1994
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Pierri, Margaret A
: REGISTRATION NUMBER: 30709
: REFERENCE/DOCKET NUMBER: STM-8
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 596-9000
: TELEFAX: (212) 596-9090
: INFORMATION FOR SEQ ID NO: 9:
: SEQUENCE CHARACTERISTICS:
```

LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-892B-9

Query Match 100.0%; Score 54; DB 7; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOKIKHVVKL 11
|||||
Db 2 KOKIKHVVKL 12

RESULT 9
US-08-996-470-1

Sequence 1, Application US/08996470A
GENERAL INFORMATION:

APPLICANT: Falk

TITLE OF INVENTION: Use of Hyaluronic Acid and Forms to Prevent Arterial
TITLE OF INVENTION: Restenosis

FILE REFERENCE:

CURRENT APPLICATION NUMBER: US/08/996,470A

CURRENT FILING DATE: 1997-12-22

EARLIER APPLICATION NUMBER: US 07/675,908

EARLIER FILING DATE: 1991-07-03

EARLIER APPLICATION NUMBER: US 07/838,674

EARLIER FILING DATE: 1992-02-21

EARLIER APPLICATION NUMBER: US 07/838,675

EARLIER FILING DATE: 1992-02-21

EARLIER APPLICATION NUMBER: US 08/125,398

EARLIER FILING DATE: 1993-09-23

EARLIER APPLICATION NUMBER: US 08/285,764

EARLIER FILING DATE: 1994-08-03

EARLIER APPLICATION NUMBER: US 07/952,095

EARLIER FILING DATE: 1992-09-28

NUMBER OF SEQ ID NOS: 2

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 1

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

NAME/KEY: BINDING

LOCATION: (1)..(12)

OTHER INFORMATION: A peptide mimicking Domain I (amino acids 401-411)

OTHER INFORMATION: of the hyaluronic acid binding region of RHAMM

US-08-996-470-1

Query Match 100.0%; Score 54; DB 13; Length 12;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOKIKHVVKL 11
|||||
Db 2 KOKIKHVVKL 12

RESULT 10
US-09-685-010-51

Sequence 51, Application US/09685010
GENERAL INFORMATION:

APPLICANT: Turley, Eva A.

APPLICANT: Cruz, Tony F.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING

TITLE OF INVENTION: CELLULAR RESPONSE TO INJURY AND OTHER PROLIFERATING CELL

FILE REFERENCE: 910130.401C1

CURRENT APPLICATION NUMBER: US/09/685,010

CURRENT FILING DATE: 2001-05-23

NUMBER OF SEQ ID NOS: 72

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 51

LENGTH: 32

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Peptide used in competition binding assay

US-09-685-010-51

Query Match 100.0%; Score 54; DB 20; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOKIKHVVKL 11
|||||
Db 1 KOKIKHVVKL 11

RESULT 11
US-09-978-309A-51

Sequence 51, Application US/09978309A
GENERAL INFORMATION:

APPLICANT: Cruz, Tony

APPLICANT: Pastrik, Aleksandra

APPLICANT: Turley, Eva A.

TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to

TITLE OF INVENTION: Injury and other Proliferating Cell Disorders Regulated by

TITLE OF INVENTION: Hyaladerlin and Hyaluronans

FILE REFERENCE: 033352-010

CURRENT APPLICATION NUMBER: US/09/978,309A

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: US 09/685,010

PRIOR FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: US 09/541,522

PRIOR FILING DATE: 2000-04-03

PRIOR APPLICATION NUMBER: US 60/127,457

PRIOR FILING DATE: 1999-04-01

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 51

LENGTH: 32

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Peptide used in competition binding assay

US-09-978-309A-51

Query Match 100.0%; Score 54; DB 23; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.025;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KOKIKHVVKL 11
|||||
Db 1 KOKIKHVVKL 11

RESULT 12
US-09-978-309A-81

Sequence 81, Application US/09978309A
GENERAL INFORMATION:

APPLICANT: Cruz, Tony

APPLICANT: Pastrik, Aleksandra

APPLICANT: Turley, Eva A.

TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to

TITLE OF INVENTION: Injury and other Proliferating Cell Disorders Regulated by

TITLE OF INVENTION: Hyaladerlin and Hyaluronans

FILE REFERENCE: 033352-010

CURRENT APPLICATION NUMBER: US/09/978,309A

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: US 09/685,010

PRIOR FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: US 09/541,522

PRIOR FILING DATE: 2000-04-03

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; PRIOR APPLICATION NUMBER: US 60/127,457
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 81
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-978-309A-81

Query Match
Best Local Similarity 100.0%; Score 54; DB 23; Length 32;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 K0K1KHVVKLK 11
Db 1 K0K1KHVVKLK 11

RESULT 13
US-09-978-309A-82
; Sequence 82, Application US/09978309A
; GENERAL INFORMATION:
; APPLICANT: Cruz, Tony
; APPLICANT: Pastrak, Aleksandra
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
; TITLE OF INVENTION: Hyaladerin and Hyaluronans
; FILE REFERENCE: 033352-010
; CURRENT APPLICATION NUMBER: US/09/978,309A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 09/685,010
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/541,522
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/127,457
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-978-309A-82

Query Match
Best Local Similarity 100.0%; Score 54; DB 23; Length 32;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 K0K1KHVVKLK 11
Db 1 K0K1KHVVKLK 11

RESULT 14
US-09-657-276-1174
; Sequence 1174, Application US/09657276
; GENERAL INFORMATION:
; APPLICANT: Conjuchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibaudau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/657,276
; CURRENT FILING DATE: 2000-09-07
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
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; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1174
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-657-276-1174

Query Match
Best Local Similarity 100.0%; Score 54; DB 20; Length 42;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 K0K1KHVVKLK 11
Db 11 K0K1KHVVKLK 21

RESULT 15
US-09-978-309A-75
; Sequence 75, Application US/09978309A
; GENERAL INFORMATION:
; APPLICANT: Cruz, Tony
; APPLICANT: Pastrak, Aleksandra
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
; TITLE OF INVENTION: Hyaladerin and Hyaluronans
; FILE REFERENCE: 033352-010
; CURRENT APPLICATION NUMBER: US/09/978,309A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 09/685,010
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/541,522
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/127,457
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 75
; LENGTH: 221
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-978-309A-75

Query Match
Best Local Similarity 100.0%; Score 54; DB 23; Length 221;
Matches 11: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 K0K1KHVVKLK 11
Db 173 K0K1KHVVKLK 183

Search completed: February 8, 2003, 10:50:49
Job time : 147.3 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2003, 10:41:35 ; Search time 16.5 Seconds

(without alignments)
54.053 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KOKIKHVYK 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 405691 seqs, 81078759 residues

Total number of hits satisfying chosen parameters: 405691

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Pending Patents_AA_New:*
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	37	68.5	272	5	US-09-134-000C-6100
2	37	68.5	272	5	US-09-134-000C-6100
3	37	68.5	272	5	US-09-134-000C-6100
4	36	66.7	234	6	US-10-092-411A-3195
5	36	66.7	284	5	US-09-134-000C-5495
6	36	66.7	284	5	US-09-134-000C-5495
7	36	66.7	1388	1	PCT-US02-21338-164
8	36	66.7	1388	6	US-10-188-832-164
9	35	64.8	188	5	US-09-950-084-4804
10	35	64.8	708	5	US-09-724-676-96355
11	35	64.8	708	5	US-09-724-676-96355
12	35	64.8	715	5	US-09-724-676-96355
13	35	64.8	715	5	US-09-724-676-96355
14	35	64.8	715	5	US-09-724-676-96355
15	35	64.8	715	5	US-09-724-676-96355
16	35	64.8	715	5	US-09-724-676-96355
17	35	64.8	715	5	US-09-724-676-96355
18	35	64.8	804	5	US-09-724-676-96355
19	35	64.8	804	5	US-09-724-676-96355
20	35	64.8	1097	6	US-10-276-774-2203
21	34	63.0	30	6	US-10-203-138A-11061
22	34	63.0	405	6	US-10-092-411A-5259
23	34	63.0	433	5	US-09-724-676-52315
24	34	63.0	433	5	US-09-724-676-52315
25	34	63.0	518	6	US-10-092-411A-4744
26	34	63.0	588	5	US-09-724-676-52313

27	34	63.0	588	5	US-09-724-676A-52313	Sequence 52313, A
28	34	63.0	655	5	US-09-724-676-71215	Sequence 71215, A
29	34	63.0	655	5	US-09-724-676-71215	Sequence 71216, A
30	34	63.0	655	5	US-09-724-676A-71215	Sequence 71215, A
31	34	63.0	655	5	US-09-724-676A-71215	Sequence 71216, A
32	34	63.0	693	1	PCT-US02-27129-5	Sequence 5, Appl
33	34	63.0	693	1	US-10-191-715-2	Sequence 2, Appl
34	34	63.0	693	6	US-10-228-063-5	Sequence 5, Appl
35	34	63.0	712	1	PCT-US02-27129-27	Sequence 27, Appl
36	34	63.0	712	6	US-10-228-063-27	Sequence 27, Appl
37	34	63.0	718	1	PCT-US02-27129-26	Sequence 26, Appl
38	34	63.0	718	1	PCT-US02-27129-36	Sequence 26, Appl
39	34	63.0	718	6	US-10-228-063-36	Sequence 26, Appl
40	34	63.0	718	6	US-10-228-063-36	Sequence 36, Appl
41	34	63.0	747	1	PCT-US02-29560-210	Sequence 210, App
42	34	63.0	747	5	US-09-724-676-52314	Sequence 52314, A
43	34	63.0	747	5	US-09-724-676A-52314	Sequence 52314, A
44	34	63.0	747	6	US-10-245-882-210	Sequence 210, App
45	34	63.0	794	6	US-10-304-095-8	Sequence 8, Appl

ALIGNMENTS

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RESULT 1
US-09-134-000C-6100
; Sequence 6100, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6100
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6100
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Query Match 68.5%; Score 37; DB 5; Length 272;
Best Local Similarity 45.5%; Pred. No. 16;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

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QY 1 KOKIKHVYK 11
Db 232 KENIEHIKVK 242

RESULT 2
US-09-134-000C-6100
; Sequence 6100, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6100
; LENGTH: 272
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-6100
```

Query Match 68.5%; Score 37; DB 5; Length 272;
Best Local Similarity 45.5%; Pred. No. 16;
Matches 5; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOKIKHVYK 11
DB 232 KENIEHVYK 242

RESULT 3

US-09-950-084-6869
; Sequence 6869, Application US/09950084
; GENERAL INFORMATION:
; APPLICANT: George H. Shimer, Jr.
; APPLICANT: George H. Miller
; APPLICANT: Roberta S. Hare
; APPLICANT: Karen J. Shaw
; TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
; FILE REFERENCE: 1034/1C963052
; CURRENT APPLICATION NUMBER: US/09/950,084
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 09/417,811
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: US 09/353,718
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/266,557
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,556
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,555
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,542
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,541
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/037,934
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/036,720
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: US 09/036,338
; PRIOR FILING DATE: 1998-03-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 7451
; SEQ ID NO 6869
; LENGTH: 624
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-950-084-6869

Query Match 68.5%; Score 37; DB 5; Length 624;
Best Local Similarity 63.6%; Pred. No. 41;
Matches 7; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 1 KOKIKHVYK 11
DB 464 RHKIRHVYK 474

RESULT 4

US-10-092-411A-3195
; Sequence 3195, Application US/10092411A
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: ENTEROMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-101
; CURRENT APPLICATION NUMBER: US/10/092,411A
; CURRENT FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: US 09/134,001
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064,964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055,779

; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5676
; SEQ ID NO 3195
; LENGTH: 234
; TYPE: PRT
; ORGANISM: Staphylococcus epidermidis
US-10-092-411A-3195

Query Match 66.7%; Score 36; DB 6; Length 234;
Best Local Similarity 77.8%; Pred. No. 21;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOKIKHVYK 9
DB 210 KPKMHVYK 218

RESULT 5

US-09-134-000C-5495
; Sequence 5495, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5495
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5495

Query Match 66.7%; Score 36; DB 5; Length 284;
Best Local Similarity 54.5%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOKIKHVYK 11
DB 244 KENIEHVYK 254

RESULT 6

US-09-134-000C-5495
; Sequence 5495, Application US/09134000C
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5495
; LENGTH: 284
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-5495

Query Match 66.7%; Score 36; DB 5; Length 284;
Best Local Similarity 54.5%; Pred. No. 26;
Matches 6; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOKIKHVYK 11
DB 244 KENIEHVYK 254

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RESULT 7
PCT-US02-21338-164.
; Sequence 164, Application PC/TUS0221338
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; TITLE OF INVENTION: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: PCT/US02/21338
; CURRENT FILING DATE: 2002-12-04
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 164
; LENGTH: 1388
; TYPE: PRT
; ORGANISM: Homo sapiens
PCT-US02-21338-164

Query Match          66.7%; Score 36; DB 1; Length 1388;
Best Local Similarity 70.0%; Pred. No. 1.Se+02;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 OKIRHVYK 11
|1111111111
Db 1351 OKIQVYVRLK 1360

RESULT 8
US-10-188-832-164
; Sequence 164, Application US/10188832
; GENERAL INFORMATION:
; APPLICANT: Mack, David H.
; APPLICANT: Aziz, Natasha
; APPLICANT: Eos Biotechnology, Inc.
; TITLE OF INVENTION: Methods of Diagnosis of Bladder Cancer, Compositions
; TITLE OF INVENTION: and Methods of Screening for Modulators of Bladder
; FILE REFERENCE: 018501-002330US
; CURRENT APPLICATION NUMBER: US/10/188,832
; CURRENT FILING DATE: 2002-11-22
; PRIOR APPLICATION NUMBER: US 60/302,814
; PRIOR FILING DATE: 2001-07-03
; PRIOR APPLICATION NUMBER: US 60/310,099
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/343,705
; PRIOR FILING DATE: 2001-11-08
; PRIOR APPLICATION NUMBER: US 60/350,666
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US 60/372,246
; NUMBER OF SEQ ID NOS: 207
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 164
; LENGTH: 1388
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-188-832-164
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Query Match          66.7%; Score 36; DB 6; Length 1388;
Best Local Similarity 70.0%; Pred. No. 1.Se+02;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 OKIRHVYK 11
|1111111111
Db 1351 OKIQVYVRLK 1360

RESULT 9
US-09-950-084-4804
; Sequence 4804, Application US/09950084
; GENERAL INFORMATION:
; APPLICANT: George H. Shimer,Jr.
; APPLICANT: George H. Miller
; APPLICANT: Roberta S. Hare
; APPLICANT: Karen J. Shaw
; TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
; FILE REFERENCE: 1034/1C9630S2
; CURRENT APPLICATION NUMBER: US/09/950,084
; CURRENT FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: US 09/417,811
; PRIOR FILING DATE: 1999-10-14
; PRIOR APPLICATION NUMBER: US 09/353,718
; PRIOR FILING DATE: 1999-07-14
; PRIOR APPLICATION NUMBER: US 09/266,557
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,556
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,555
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,542
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/266,541
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/037,934
; PRIOR FILING DATE: 1998-03-10
; PRIOR APPLICATION NUMBER: US 09/036,720
; PRIOR FILING DATE: 1998-03-06
; PRIOR APPLICATION NUMBER: US 09/036,338
; PRIOR FILING DATE: 1998-03-06
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 7451
; SEQ ID NO 4804
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-950-084-4804

Query Match          64.8%; Score 35; DB 5; Length 188;
Best Local Similarity 66.7%; Pred. No. 26;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 OKIRHVYK 10
|1111111111
Db 100 QIRHVAKI 108

RESULT 10
US-09-724-676-96355
; Sequence 96355, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: Patentln version 3.2
; SEQ ID NO 96355
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-96355
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US-09-724-676-96355

Query Match

64.8%: Score 35; DB 5; Length 708;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVRLK 11

Db 127 KIPHVRLK 135

RESULT 11

US-09-724-676A-96355
; Sequence 96355, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96355
; LENGTH: 708
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-96355

Query Match

64.8%: Score 35; DB 5; Length 708;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVRLK 11

Db 127 KIPHVRLK 135

RESULT 12

US-09-724-676-96353
; Sequence 96353, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96353
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676-96353

Query Match

64.8%: Score 35; DB 5; Length 715;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVRLK 11

Db 127 KIPHVRLK 135

RESULT 13

US-09-724-676-96354
; Sequence 96354, Application US/09724676
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222

; SOFTWARE: PatentIn version 3.2

; SEQ ID NO 96354

; LENGTH: 715

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-724-676-96354

Query Match

64.8%: Score 35; DB 5; Length 715;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVRLK 11

Db 127 KIPHVRLK 135

RESULT 14

US-09-724-676A-96353
; Sequence 96353, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96353
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-96353

Query Match

64.8%: Score 35; DB 5; Length 715;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVRLK 11

Db 127 KIPHVRLK 135

RESULT 15

US-09-724-676A-96354
; Sequence 96354, Application US/09724676A
; GENERAL INFORMATION:
; APPLICANT: Compugen LTD
; TITLE OF INVENTION: Variants of alternative splicing
; FILE REFERENCE: 129181.4 Compugen
; CURRENT APPLICATION NUMBER: US/09/724,676A
; CURRENT FILING DATE: 2000-11-28
; NUMBER OF SEQ ID NOS: 97222
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 96354
; LENGTH: 715
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-724-676A-96354

Query Match

64.8%: Score 35; DB 5; Length 715;
Best Local Similarity 77.8%; Pred. No. 1.1e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVRLK 11

Db 127 KIPHVRLK 135

Search completed: February 8, 2003, 10:51:42
Job time : 18.5 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:39:30 ; Search time 12.4667 Seconds
(without alignments)
25.961 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KOKIKHVYK 11

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
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4: /cgn2_6/ptodata/1/laa/6B.COMB.pep: *
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6: /cgn2_6/ptodata/1/laa/backfiles1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	54	100.0	32	4	US-08-477-831C-38
2	54	100.0	183	4	US-08-477-831C-41
3	54	100.0	351	1	US-08-402-217A-2
4	54	100.0	351	1	US-08-700-178-2
5	54	100.0	351	3	US-08-995-654-2
6	54	100.0	477	1	US-08-402-217A-3
7	54	100.0	477	1	US-08-700-178-3
8	54	100.0	477	3	US-08-995-654-3
9	54	100.0	606	4	US-08-477-831C-2
10	54	100.0	631	4	US-08-477-831C-11
11	51	94.4	183	4	US-08-477-831C-40
12	46	85.2	32	4	US-08-477-831C-39
13	36	66.7	234	4	US-09-134-001C-3195
14	36	66.7	1388	4	US-09-572-191-2
15	36	66.7	1388	4	US-09-723-262-2
16	36	66.7	1388	4	US-09-723-219-2
17	34	63.0	196	2	US-08-933-750C-35
18	34	63.0	196	4	US-09-234-613-35
19	34	63.0	373	4	US-09-586-875-1
20	34	63.0	405	4	US-09-134-001C-5259
21	34	63.0	518	4	US-09-134-001C-4744
22	34	63.0	655	1	US-08-264-002-2
23	33	61.1	437	4	US-09-134-001C-5396
24	33	61.1	456	1	US-08-021-601-6
25	33	61.1	456	1	US-08-082-849B-6
26	33	61.1	456	5	PCT-US94-01624-6
27	33	61.1	472	1	US-08-021-601-8

28	33	61.1	472	1	US-08-082-849B-8	Sequence 8, Appli
29	33	61.1	472	5	PCT-US94-01624-8	Sequence 8, Appli
30	33	61.1	508	1	US-08-021-601-10	Sequence 10, Appli
31	33	61.1	508	1	US-08-082-849B-10	Sequence 10, Appli
32	33	61.1	508	5	PCT-US94-01624-10	Sequence 10, Appli
33	33	61.1	776	1	US-08-021-601-2	Sequence 2, Appli
34	33	61.1	776	1	US-08-082-849B-2	Sequence 2, Appli
35	33	61.1	776	5	PCT-US94-01624-2	Sequence 2, Appli
36	33	61.1	1024	4	US-09-562-737-83	Sequence 83, Appli
37	33	61.1	2005	3	US-08-836-325-7	Sequence 7, Appli
38	33	61.1	3248	1	US-08-353-700-1	Sequence 1, Appli
39	33	61.1	3248	5	PCT-US95-16216-1	Sequence 1, Appli
40	32	59.3	70	4	US-09-367-953B-53	Sequence 53, Appli
41	32	59.3	70	4	US-09-367-953B-72	Sequence 72, Appli
42	32	59.3	99	1	US-08-004-492-9	Sequence 9, Appli
43	32	59.3	281	4	US-09-404-258-17	Sequence 17, Appli
44	32	59.3	290	4	US-09-071-035-96	Sequence 96, Appli
45	32	59.3	307	4	US-09-134-001C-5144	Sequence 5144, Ap

ALIGNMENTS

RESULT 1
US-08-477-831C-38
; Sequence 38, Application US/08477831C
; Patent No. 6429291
; GENERAL INFORMATION:
; APPLICANT: TURLEY, EVA A.
; APPLICANT: SHUMEN, ZHANG
; APPLICANT: ENTWISTLE, JOYCELYN
; TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Rel. #1.0, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,831C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PIERRI, MARGARET A.
; REGISTRATION NUMBER: 30,709
; REFERENCE/DOCKET NUMBER: SIM-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: /desc = protein fragment
US-08-477-831C-38

Query Match 100.0%; Score 54; DB 4; Length 32;
Best Local Similarity 100.0%; Pred. No. 0.0039;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 KOKIKHVYK 11
|||
Db 1 KOKIKHVYK 11

RESULT 2
US-08-477-831C-41
; Sequence 41, Application US/08477831C
; Patent No. 6429291
; GENERAL INFORMATION:
; APPLICANT: TURLEY, EVA A.
; APPLICANT: SHUMEN, ZHANG
; APPLICANT: ENTWISTLE, JOYCELYN
; TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Rel. #1.0, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,831C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PIERRI, MARGARET A.
; REGISTRATION NUMBER: 30,709
; REFERENCE/DOCKET NUMBER: STM-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 41:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 183 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE:
; DESCRIPTION: /desc = protein fragment
; US-08-477-831C-41
Query Match 100.0%; Score 54; DB 4; Length 183;
Best Local Similarity 100.0%; Pred. No. 0.022;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KOKIKHVVKL 11
Db 166 KOKIKHVVKL 176
RESULT 3
US-08-402-217A-2
; Sequence 2, Application US/08402217A
; Patent No. 5587301
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Sellhammer, Jeffrey J.
; TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
; TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,217A
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF-002805
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-402-217A-2
Query Match 100.0%; Score 54; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 KOKIKHVVKL 11
Db 318 KOKIKHVVKL 328
RESULT 4
US-08-700-178-2
; Sequence 2, Application US/08700178
; Patent No. 5783669
; Patent No. 5783669 5700912
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Sellhammer, Jeffrey J.
; TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
; TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,178
; FILING DATE: August 20, 1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/402,217
; FILING DATE: March 10, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0028-1 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-845-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-700-178-2

Query Match 100.0%; Score 54; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOKIKHVVKLK 11
|||||
Db 318 KOKIKHVVKLK 328

RESULT 5
US-08-995-654-2
; Sequence 2, Application US/08995654
; Patent No. 6025138
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig
; APPLICANT: Sellhammer, Jeffrey
; TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
; TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,654
; FILING DATE: December 22, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/700,178
; FILING DATE: August 20, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402,217
; FILING DATE: March 10, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0028-2 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 351 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-995-654-2

Query Match 100.0%; Score 54; DB 3; Length 351;
Best Local Similarity 100.0%; Pred. No. 0.043;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOKIKHVVKLK 11
|||||
Db 318 KOKIKHVVKLK 328

RESULT 6

US-08-402-217A-3
; Sequence 3, Application US/08402217A
; Patent No. 5587301
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Sellhammer, Jeffrey J.
; TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
; TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,217A
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF-0028US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; LIBRARY: mouse
; CLONE: GI 53979
US-08-402-217A-3

Query Match 100.0%; Score 54; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOKIKHVVKLK 11
|||||
Db 402 KOKIKHVVKLK 412

RESULT 7
US-08-700-178-3
; Sequence 3, Application US/08700178
; Patent No. 5783669
; Patent No. 5783669 5700912
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Sellhammer, Jeffrey J.
; TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
; TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,178
; FILING DATE: August 20, 1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/402,217
; FILING DATE: March 10, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0028-1 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; LIBRARY: mouse
; CLONE: GI 53979
;
US-08-700-178-3

```

```

Query Match          100.0%; Score 54; DB 1; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```
OY 1 KOKIKHVVKLK 11
DB 402 KOKIKHVVKLK 412

```

```

RESULT 8
US-08-995-654-3
; Sequence 3, Application US/08995654
; Patent No. 6025138
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig
; APPLICANT: Sellhammer, Jeffrey
; TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
; TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: Windows
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,654
; FILING DATE: December 22, 1997
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/700,178
; FILING DATE: August 20, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/402,217
; FILING DATE: March 10, 1995
;

```

```

; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0028-2 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
US-08-995-654-3

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Query Match          100.0%; Score 54; DB 3; Length 477;
Best Local Similarity 100.0%; Pred. No. 0.058;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
OY 1 KOKIKHVVKLK 11
DB 402 KOKIKHVVKLK 412

```

```

RESULT 9
US-08-477-831C-2
; Sequence 2, Application US/08477831C
; Patent No. 6429291
; GENERAL INFORMATION:
; APPLICANT: TURLEY, EVA A.
; APPLICANT: SHUMEN, ZHANG
; APPLICANT: ENTWISTLE, JOYCELYN
; TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10020-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Rel. #1.0, ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,831C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PIERRE, MARGARET A.
; REGISTRATION NUMBER: 30,709
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9090
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 606 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: /desc = "RHAMM I protein"
;
US-08-477-831C-2

```

```

Query Match          100.0%; Score 54; DB 4; Length 606;
Best Local Similarity 100.0%; Pred. No. 0.074;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```
OY 1 KOKIKHVVKLK 11

```


TOPOLOGY: linear
 MOLECULE TYPE:
 DESCRIPTION: /desc - protein fragment
 US-08-477-831C-39

Query Match 85.2%; Score 46; DB 4; Length 32;
 Best Local Similarity 81.8%; Pred. No. 0.093;
 Matches 9; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOKIKHVYK 11
 |||:|:|:|
 Db 1 KOKIKHVYELK 11

RESULT 13
 US-09-134-001C-3195
 : Sequence 3195, Application US/09134001C
 : Patent No. 6380370
 : GENERAL INFORMATION:
 : APPLICANT: Lynn Doucette-Stamm et al
 : TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 : FILE REFERENCE: GTC-007
 : CURRENT APPLICATION NUMBER: US/09/134,001C
 : PRIOR FILING DATE: 1998-08-13
 : PRIOR APPLICATION NUMBER: US 60/064,964
 : PRIOR FILING DATE: 1997-11-08
 : PRIOR APPLICATION NUMBER: US 60/055,779
 : PRIOR FILING DATE: 1997-08-14
 : NUMBER OF SEQ ID NOS: 5674
 : SEQ ID NO 3195
 : LENGTH: 234
 : TYPE: PRT
 : ORGANISM: Staphylococcus epidermidis
 US-09-134-001C-3195

Query Match 66.7%; Score 36; DB 4; Length 224;
 Best Local Similarity 77.8%; Pred. No. 35;
 Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOKIKHVYK 9
 |:|:|:|:|
 Db 210 KKKKHHVYK 218

RESULT 14
 US-09-572-191-2
 : Sequence 2, Application US/09572191
 : Patent No. 6355466
 : GENERAL INFORMATION:
 : APPLICANT: Beraud, Christophe
 : APPLICANT: Sakowicz, Roman
 : APPLICANT: Wood, Kenneth
 : TITLE OF INVENTION: No. 63554661 motor proteins and methods for
 : FILE REFERENCE: 1017
 : CURRENT APPLICATION NUMBER: US/09/572,191
 : CURRENT FILING DATE: 2000-05-17
 : NUMBER OF SEQ ID NOS: 6
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 2
 : LENGTH: 1388
 : TYPE: PRT
 : ORGANISM: Human
 US-09-572-191-2

Query Match 66.7%; Score 36; DB 4; Length 1388;
 Best Local Similarity 70.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 OKIKHVYK 11
 |||:|:|:|
 Db 1351 OKIQVYVRLK 1360

RESULT 15
 US-09-723-262-2
 : Sequence 2, Application US/09723262
 : Patent No. 6379912
 : GENERAL INFORMATION:
 : APPLICANT: Beraud, Christophe
 : APPLICANT: Sakowicz, Roman
 : APPLICANT: Wood, Kenneth
 : TITLE OF INVENTION: No. 6379912el motor proteins and methods for
 : FILE REFERENCE: 1017
 : CURRENT APPLICATION NUMBER: US/09/723,262
 : CURRENT FILING DATE: 2000-11-27
 : PRIOR APPLICATION NUMBER: US 09/572,191
 : PRIOR FILING DATE: 2000-05-17
 : NUMBER OF SEQ ID NOS: 6
 : SOFTWARE: FastSeq for Windows Version 4.0
 : SEQ ID NO 2
 : LENGTH: 1388
 : TYPE: PRT
 : ORGANISM: Human
 US-09-723-262-2

Query Match 66.7%; Score 36; DB 4; Length 1388;
 Best Local Similarity 70.0%; Pred. No. 2.1e+02;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 OKIKHVYK 11
 |||:|:|:|
 Db 1351 OKIQVYVRLK 1360

Search completed: February 8, 2003, 10:44:04
 Job time : 13.4667 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:39:10 ; Search time 12 Seconds
(without alignments)
80.112 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KLUKSQLVXK 10

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283224 seqs, 96134422 residues
Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 73:.*
1: p1r1:.*
2: p1r2:.*
3: p1r3:.*
4: p1r4:.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	93.5	631	2 JCA4298	hyaluronan recepto
2	38	82.6	640	1 A86657	fructose-bisphosph
3	37	80.4	336	2 T30161	hypothetical prote
4	35	76.1	302	2 A34406	aldehyde reductase
5	35	76.1	316	1 A60603	aldehyde reductase
6	35	76.1	316	2 T40984	aldehyde reductase
7	35	76.1	456	2 T40898	aldehyde reductase
8	34	73.9	34	2 T70239	pyruvate dehydroge
9	34	73.9	306	2 D71696	hypothetical prote
10	34	73.9	362	2 B64527	penicillin-binding
11	34	73.9	522	2 T28323	M-protein - Helico
12	34	73.9	633	2 D75112	ORF MSY162 probabl
13	34	73.9	874	4 GNMUER	glu-tRNA amidotran
14	34	73.9	1785	2 A45546	retrovirus-related
15	34	73.9	2145	2 S61041	major mezozole su
16	33	71.7	82	2 T51682	glutamate synthase
17	33	71.7	99	2 A42196	myb-related transac
18	33	71.7	159	2 C83096	preprotein translo
19	33	71.7	261	2 T06650	conserved hypothet
20	33	71.7	404	2 A97559	myb-related protei
21	33	71.7	404	2 A82779	hypothetical prote
22	33	71.7	431	1 BWMSSV	acetyltransferase [i
23	33	71.7	431	2 S30116	preprotein translo
24	33	71.7	431	2 S65157	hypothetical translo
25	33	71.7	455	2 S65157	hypothetical prote
26	33	71.7	1480	2 T21911	hypothetical prote
27	33	71.7	1483	2 T21912	hypothetical prote
28	32	69.6	113	2 C89828	hypothetical prote
29	32	69.6	176	2 AD1226	conserved hypothet
					hypothetical prote

30	32	69.6	176	2 AF1579	hypothetical prote
31	32	69.6	301	2 F90115	beta subunit of G
32	32	69.6	316	1 A39763	aldehyde reductase
33	32	69.6	405	2 T10630	ethylene-regulated
34	32	69.6	490	2 T21457	hypothetical prote
35	32	69.6	584	2 C84045	hypothetical prote
36	32	69.6	589	2 B29514	pyruvate kinase py
37	32	69.6	589	2 A29476	muscarinic acetylch
38	32	69.6	590	2 S10128	muscarinic acetylch
39	32	69.6	590	2 S01114	muscarinic acetylch
40	32	69.6	590	2 S47572	PTS mannitol-speci
41	32	69.6	610	2 B69661	hypothetical prote
42	32	69.6	635	2 D86265	hypothetical prote
43	32	69.6	639	2 A55019	muscarinic acetylch
44	32	69.6	725	2 A47168	cardiac morphogene
45	32	69.6	772	2 T01061	hypothetical prote

ALIGNMENTS

RESULT 1

JC4298

hyaluronan receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 16-Nov-1995 #sequence_revastion 08-Feb-1996 #ext_change 01-Dec-2000

C:Accession: JC4298; A42925; A41923; S21586

R:Entwistle, J.; Zhang, S.; Yang, B.; Wong, C.; Li, Q.; Hall, C.L.; A, U.; Mowat, M.; G

Gene 163, 233-238, 1995

A:Title: Characterization of the murine gene encoding the hyaluronan receptor RHAMM.

A:Reference number: JC4298; MUID:96011639; PMID:7590272

A:Accession: JC4298

A:Molecule type: mRNA

A:Residues: 1-631 <ENT>

A:Cross-references: EMBL:X64550

A:Experimental source: 3T3 fibroblast

R:Hardwick, C.

J. Cell Biol. 118, 753, 1992

A:Reference number: A42925; MUID:92348516; PMID:1639856

A:Contents: erratum

A:Accession: A42925

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 155-376, 'S', 378-504, 'E', 506-631 <HAR>

A:Cross-references: GB:X64550

A>Note: authors translated the codon AGT for residue 377 as Thr and CTA for residue 507 &

R:Hardwick, C.; Hoare, K.; Owens, R.; Hohn, H.P.; Hook, M.; Moore, D.; Cripps, V.; Auster

J. Cell Biol. 117, 1343-1350, 1992

A:Title: Molecular cloning of a novel hyaluronan receptor that mediates tumor cell motility

A:Reference number: A41923; MUID:92299690; PMID:1376732

A:Accession: A41923

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 155-376, 'S', 378-504, 'E', 506-507, 'L', 508-630 <HA2>

A:Cross-references: GB:X64550

A>Note: this sequence has been corrected in reference A42925

C:Comment: This protein regulates cell motility and transformation, and focal adhesion d

C:Genetics:

A:Gene: rhann

A:Inserts: 20/3; 54/2; 79/2; 137/3; 187/3; 259/2; 382/2; 431/2; 482/2; 515/3; 574/3; 625/

C:Superfamily: hyaluronan receptor

C:Keywords: glycoprotein; receptor

F:260-382/Region: 21 residue repeats

F:516-574/Region: hyaluronan binding #status predicted

F:575-625/Region: hyaluronan binding #status predicted

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

F:116,283,304,325,346,367,398,438,619/Binding site: carbohydrate (Asn) (covalent) #status

Query Match 93.5%; Score 43; DB 2; Length 631;
Best Local Similarity 90.0%; Pred. No. 1;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Db 578 KLRSQLVKKR 587

RESULT 2

A:fructose-bisphosphatase (EC 3.1.3.11) [similarity] - Lactococcus lactis subsp. lactis (E
A:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 11-Jan-2002
C:Accession: A86657
R:Bojoltin, A.; Winkler, P.; Mauger, S.; Jallion, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis s
A:Reference number: A86657; MUID:21235186; PMID:11337471
A:Accession: A86657
A:Molecule type: DNA
A:Residues: 1-640 <STO>
A:Cross-references: GB:AE005176; PID:g12723117; PIDN:AAK04355.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: fbp
C:Function:
A:Description: catalyzes the hydrolysis of fructose-1,6-bisphosphate to fructose-6-phosp
A:Pathway: Gluconeogenesis
C:Superfamily: Bacillus subtilis fructose-bisphosphatase; phosphoesterase core homology
C:Keywords: carbohydrate metabolism; gluconeogenesis; metalloprotein; phosphoric monoes

Query Match 82.6%; Score 38; DB 1; Length 640;
Best Local Similarity 70.0%; Pred. No. 11;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLRSQLVKKR 10
Db 311 KLRSQLVKKR 320

RESULT 3

A:hypothetical protein C37A2.8 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T30161
R:Lee, T.T.; Kemp, K.; Scheet, P.
submitted to the EMBL Data Library, April 1997
A:Description: The sequence of C. elegans cosmid C37A2.
A:Reference number: Z20746
A:Accession: T30161
A:Molecule type: protein
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-336 <LET>
A:Cross-references: EMBL:U97194; PIDN:AAH52452.1; GSPDB:GN00019; CESP:C37A2.8
A:Experimental source: strain Bristol N2; clone C37A2
C:Genetics:
A:Gene: CESP:C37A2.8
A:Map position: 1
A:introns: 42/3; 77/3; 198/1; 264/1; 295/3

Query Match 80.4%; Score 37; DB 2; Length 336;
Best Local Similarity 70.0%; Pred. No. 8.9;
Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLRSQLVKKR 10
Db 48 KLRSQLVKKR 57

RESULT 4

A:aldehyde reductase (EC 1.1.1.21) - rabbit (fragment)
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 22-Jun-1990 #sequence_revision 22-Jun-1990 #text_change 11-Jun-1999
C:Accession: A34406
R:Garca-Perez, A.; Martin, B.; Murphy, H.R.; Uchida, S.; Murer, H.; Cowley Jr., B.D.; H
J. Biol. Chem. 264, 16815-16821, 1989

A:Title: Molecular cloning of cDNA coding for kidney aldose reductase. Regulation of spe
A:Reference number: A34406; MUID:89380313; PMID:2506183
A:Accession: A34406
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-302 <GAR>
A:Cross-references: GB:U05048; NID:g164756; PIDN:AAA31157.1; PID:g164757
C:Superfamily: aldehyde reductase
C:Keywords: oxidoreductase

Query Match 76.1%; Score 35; DB 2; Length 302;
Best Local Similarity 70.0%; Pred. No. 20;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLRSQLVKKR 10
Db 48 KLRSQLVKKR 57

RESULT 5

A:aldehyde reductase (EC 1.1.1.21) - rat
A:Accession: A60603
N:Alternate names: aldose reductase
C:Species: Rattus norvegicus (Norway rat)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: A60603; S00079; B60603; I53649
R:Carper, D.A.; Wistow, G.; Nishimura, C.; Graham, C.; Watanabe, K.; Fujii, Y.; Hayashi,
Exp. Eye Res. 49, 377-388, 1989
A:Title: A superfamily of NADPH-dependent reductases in eukaryotes and prokaryotes.
A:Reference number: A60603; MUID:90005742; PMID:2507340
A:Accession: A60603
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-316 <CAR>
R:Carper, D.; Nishimura, C.; Shinohara, T.; Dietzhold, B.; Wistow, G.; Craft, C.; Kador
FEBS Lett. 220, 209-213, 1987
A:Title: Aldose reductase and rho-crystallin belong to the same protein superfamily as a
A:Reference number: S00079; MUID:87276556; PMID:3111886
A:Accession: S00079
A:Molecule type: mRNA
A:Residues: 33-316 <CA2>
A:Cross-references: EMBL:X05884
A:Note: 45-Ser and 54-Trp were also found
A:Accession: B60603
A:Molecule type: protein
A:Residues: 34-60, 'XXX', 92-108, 146-173, 204-231, 244-252, 276-294 <CA3>
A:Note: part of this sequence was confirmed by protein sequencing
R:Graham, C.B.; Szpirer, C.; Levan, G.; Carper, D.
Gene 107, 259-267, 1991
A:Title: Characterization of the aldose reductase-encoding gene family in rat.
A:Reference number: I53649; MUID:92084118; PMID:1748296
A:Accession: I53649
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-316 <RES>
A:Cross-references: GB:M60322; NID:g202851; PIDN:AAA40721.1; PID:g202852
C:Comment: Aldose reductase catalyzes reduction of a variety of sugars to sugar alcohols
C:Comment: This enzyme is active in the eye lens, where an accumulation of sugar alcohol
C:Genetics:
A:introns: 22/3; 76/3; 117/3; 143/3; 184/3; 220/2; 247/3; 275/3; 303/2
C:Superfamily: aldehyde reductase
C:Keywords: eye lens; NADP; oxidoreductase
F:263/Active site: Lys #status predicted

Query Match 76.1%; Score 35; DB 1; Length 316;
Best Local Similarity 70.0%; Pred. No. 21;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLRSQLVKKR 10
Db 62 KLRSQLVKKR 71


```

RESULT 6
149484
A:Idenhyde reductase (EC 1.1.1.21) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: 149484
R:Gu, T.; Yamamoto, T.; Kokai, Y.; Nishimura, C.
Eur. J. Biochem. 227, 448-453, 1995
A:Title: Presence of a closely related subgroup in the aldo-ketoreductase family of the
A:Reference number: 149484; MUID:95154325; PMID:7851421
A:Accession: 149484
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-316 <RES>
A:Cross-references: GB:D32250; NID:g1384073; PIDN:BAA06980.1; PID:g786001
C:Superfamily: aldehyde reductase
C:Keywords: NADP; oxidoreductase

Query Match
Best Local Similarity 76.1%; Score 35; DB 2; Length 316;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIKSOLVKRK 10
Db 62 KIKSQVVKRKQ 71

RESULT 7
140898
pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase component [similarity]
C:Species: Schizosaccharomyces pombe
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 19-Jan-2001
C:Accession: T40898; T43185
R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Botte, G.; Pohl, T.
submitted to the EMBL Data Library, December 1998
A:Reference number: 221955
A:Accession: T40898
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-456 <MOO>
A:Cross-references: EMBL:AL034564; NID:g4049533; PIDN:CAA2547.1; PID:g4049542; GSPDB:GN
A:Experimental source: strain 972h-; cosmid c1259
R:Yoshioaka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A:Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A:Reference number: Z17323; MUID:98162722; PMID:9501991
A:Accession: T43185
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 94-174; 'N', 176-177, 'D', 179-181, 'DRKPVVSCYRPSGSPQRCIKHTSDKLIKGLFLFKNLFF',
A:Cross-references: EMBL:D89260; NID:g1749727; PIDN:BAA13921.1; PID:g1749728
A:Experimental source: strain PR745
C:Genetics:
A:Gene: SPDB:SPCC1259.09c
A:Map position: 3
A:Introns: 25/1; 60/1; 75/1; 285/1; 362/2
C:Superfamily: pyruvate dehydrogenase complex protein X; lipoyl/biotin-binding homology

Query Match
Best Local Similarity 80.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KIKSOLVKRK 10
Db 275 KIKSLIAKRK 284

RESULT 8
E70239
hypothetical protein BBH39 - Lyme disease spirochete plasmid H/1p28-3
C:Species: Borrelia burgdorferi (Lyme disease spirochete)
C:Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999
C:Accession: E70239

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R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lachigra, R.; White
son, D.; Peterson, J.; Kerville, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt,
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.
Nature 390, 580-586, 1997
A:Authors: Smith, H.O.; Venter, J.C.
A:Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.
A:Reference number: A70100; MUID:98065943; PMID:9403685
A:Accession: E70239
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-34 <KLE>
A:Cross-references: GB:AE000784; NID:g2690041; PIDN:MAC66012.1; PID:g2690068; TIGR:BBH39
A:Experimental source: strain B31
C:Genetics:
A:Genome: plasmid

Query Match
Best Local Similarity 73.9%; Score 34; DB 2; Length 34;
Matches 5; Conservative 5; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KIKSOLVKRK 10
Db 12 KIKMLIKRK 21

RESULT 9
D71696
penicillin-binding protein dacF precursor (dacF) RP389 - Rickettsia prowazekii
C:Species: Rickettsia prowazekii
C:Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000
C:Accession: D71696
R:Anderson, S.G.R.; Zomorodipour, A.; Anderson, J.O.; Sichteritz-Ponten, T.; Alemark, U
Nature 396, 133-140, 1998
A:Title: The genome sequence of Rickettsia prowazekii and the origin of mitochondria.
A:Reference number: A71630; MUID:99039499; PMID:9823893
A:Accession: D71696
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-306 <AND>
A:Cross-references: GB:AJ235271; GB:AJ235269; NID:g3868717; PIDN:CAA14846.1; PID:g386094;
A:Experimental source: strain Madrid E
C:Genetics:
A:Gene: dacF; RP389

Query Match
Best Local Similarity 73.9%; Score 34; DB 2; Length 306;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KIKSOLVKRK 10
Db 293 KAKSKIIKRK 302

RESULT 10
B64527
M-protein - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 30-Jan-1998 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C:Accession: B64527
R:Tom, J.F.; White, O.; Karlavage, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khakhria, H.G.; Glodex, A.; McKenney
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L.
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karp, P.D.; Smith, H.O.; Fraser, C.J.
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: B64527
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-362 <TOM>
A:Cross-references: GB:AE000511; TIGR:HP0058

Query Match
Best Local Similarity 73.9%; Score 34; DB 2; Length 362;

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Best Local Similarity 70.0%; Pred. No. 39;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKSQLVKRR 10
|:|:|:|:|
Db 204 KKSRLVKRR 213

RESULT 11

ORF M5V162 probable NAD+ dependent DNA ligase - Melanoplus sanguinipes entomopoxvirus
T28323
C/Species: Melanoplus sanguinipes entomopoxvirus
C/Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000
C/Accession: T28323
R/Alfonso, C.L.; Tulman, E.R.; Lu, Z.; Oma, E.; Kurish, G.F.; Rock, D.L.
J. Virol. 73, 533-552, 1999
A/Title: The genome of Melanoplus sanguinipes entomopoxvirus.
A/Reference number: Z20484; MUID:99102612; PMID:9847359
A/Accession: T28323
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-522 <AFO>
A/Cross-references: EMBL:AF063866; NID:94049647; PIDN:AA097679.1; PID:94049719
C/Genetics:
A/Note: M5V162

Query Match 73.9%; Score 34; DB 2; Length 522;
Best Local Similarity 60.0%; Pred. No. 56;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKSQLVKRR 10
|:|:|:|:|
Db 500 KKSRLVKRR 509

RESULT 12

glu-tRNA amidotransferase, chain B (gabB) PAB1902 - Pyrococcus abyssi (strain Orsay)
D75112
C/Species: Pyrococcus abyssi
C/Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Aug-1999
C/Accession: D75112
R/Anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A/Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome turn
A/Reference number: A75001
A/Accession: D75112
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-633 <KAM>
A/Cross-references: GB:AJ248285; GB:AL096836; NID:95458067; PIDN:CA849613.1; PID:el51550
C/Genetics:
A/Genes: PAB1902

Query Match 73.9%; Score 34; DB 2; Length 633;
Best Local Similarity 70.0%; Pred. No. 68;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KKSQLVKRR 10
|:|:|:|:|
Db 617 KKSQIVRRK 626

RESULT 13

retrovirus-related pol polyprotein pseudogene - human
CNHUR
N/Contains: endonuclease (EC 3.1.-.-); RNA-directed DNA polymerase (EC 2.7.7.49)
C/Species: Homo sapiens (man)
C/Date: 28-Dec-1987 #sequence_revision 04-Jan-1996 #text_change 14-May-1999
C/Accession: D24483
R/Ono, K.; Yasunaga, T.; Miyata, T.; Ushikubo, H.
J. Virol. 60, 589-598, 1986
A/Title: Nucleotide sequence of human endogenous retrovirus genome related to the mouse

A/Reference number: A93023; MUID:87036922; PMID:3021993
A/Accession: D24483
A/Status: conceptual translation of pseudogene
A/Molecule type: DNA
A/Residues: 1-874 <ONO>
A/Cross-references: GB:M14123; NID:9182227
C/Genetics:
A/Genes: POL

C/Keywords: endonuclease; hydrolase; nucleotidyltransferase; polypeptide; pseudogene; re
F:35-250/Domain: RNA-directed DNA polymerase <REV>
F:585-764/Domain: endonuclease <END>

Query Match 73.9%; Score 34; DB 4; Length 874;
Best Local Similarity 77.8%; Pred. No. 93;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 LKSQLVKRR 10
|:|:|:|:|
Db 752 LKTVLVKRR 760

RESULT 14

major merozoite surface antigen precursor - Plasmodium chabaudi chabaudi
A45546
C/Species: Plasmodium chabaudi chabaudi
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 26-Aug-1999
C/Accession: A45546
R/Deleerijder, W.; Hendrix, D.; Bendahan, N.; Hanegreets, J.; Brjls, L.; Hamers-Caste
Mol. Biochem. Parasitol. 43, 231-244, 1990
A/Title: Molecular cloning and sequence analysis of the gene encoding the major merozoite
A/Reference number: A45546; MUID:9121805; PMID:2090945
A/Accession: A45546
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-1785
A/Cross-references: GB:M34947; NID:9160597; PID:9160598
A/Superfamily: major merozoite surface antigen
C/Keywords: surface antigen

Query Match 73.9%; Score 34; DB 2; Length 1785;
Best Local Similarity 77.8%; Pred. No. 1.9e+02;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 LKSQLVKRR 10
|:|:|:|:|
Db 1180 LKSRLVKRR 1188

RESULT 15

glutamate synthase (NADH2) (EC 1.4.1.14) gltI precursor (similarity) - yeast (Saccharomy
S61041
N/Alternate names: protein D1448; protein YDL171C
C/Species: Saccharomyces cerevisiae
C/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 03-Jun-2002
R/Pohl, T.M.
Submitted to the EMBL Data Library, November 1995
A/Reference number: S61041
A/Accession: S61041
A/Molecule type: DNA
A/Residues: 1-2145 <POH>
A/Cross-references: EMBL:Z67750; NID:91061256; PIDN:CAA91574.1; PID:91061267
R/Pohl, T.M.
Submitted to the Protein Sequence Database, July 1996
A/Reference number: S67708
A/Accession: S67723
A/Molecule type: DNA
A/Residues: 1-2145 <POW>
A/Cross-references: EMBL:Z74219; NID:91431273; PIDN:CAA98745.1; PID:91431274; MIPS:YDL17
A/Experimental source: strain S288C
C/Genetics:
A/Genes: SGD:GLT1
A/Cross-references: SGD:S0002330; MIPS:YDL171C

A;Map position: 4L
 C;Superfamily: glutamate synthase (NADH)
 C;Keywords: 3fe-4S; metalloprotein; oxidoreductase; transmembrane protein
 F:1-53/Domain: propeptide #status predicted <PRO>
 F:54-2145/Product: glutamate synthase #status predicted <MAT>
 F:1077-1093/Domain: transmembrane #status predicted <TM1>
 F:1172-1188/Domain: transmembrane #status predicted <TM2>
 F:54/Active site: Cys #status predicted
 F:1185,1191,1196/Binding site: 3fe-4S cluster (Cys) (covalent) #status predicted

Query Match 73.9%; Score 34; DB 2; Length 2145;
 Best Local Similarity 70.0%; Pred.No. 2.3e+02;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLKSQLVKRK 10
 DB 464 KLKSQLVKRK 473

Search completed: February 8, 2003, 10:43:26
 Job time : 14 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:36:15 ; Search time 6.33333 Seconds
(without alignments)
65.489 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KLSQVYRK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	43	93.5	794	1 HMMR_MOUSE	Q00547 mus musculus
2	39	84.8	498	1 HMMR_RAT	P97779 rattus norv
3	35	76.1	315	1 ALDR_MOUSE	P45376 mus musculus
4	35	76.1	315	1 ALDR_RABIT	P15122 oryctolagus
5	35	76.1	315	1 ALDR_RAT	P07943 rattus norv
6	34	73.9	874	1 POLI_HUMAN	P10266 homo sapien
7	34	73.9	2144	1 GLT1_YEAST	Q12680 saccharomyc
8	33	71.7	99	1 SECY_BACST	P28620 bacillus st
9	33	71.7	431	1 SECY_BACLI	Q05207 bacillus st
10	33	71.7	455	1 SECY_BACST	P16336 bacillus st
11	33	71.7	455	1 YP46_YEAST	Q12080 saccharomyc
12	32	69.6	315	1 ALDR_HUMAN	P15121 homo sapien
13	32	69.6	589	1 ACW3_MOUSE	Q09233 mus musculus
14	32	69.6	589	1 ACW3_RAT	P04883 rattus norv
15	32	69.6	590	1 ACW3_BOVIN	P41984 bos taurus
16	32	69.6	590	1 ACW3_GORGO	Q09243 gorilla gor
17	32	69.6	590	1 ACW3_HUMAN	P20309 homo sapien
18	32	69.6	590	1 ACW3_PANTR	Q09244 pan troglod
19	32	69.6	590	1 ACW3_PIG	P11483 sus scrofa
20	32	69.6	590	1 ACW3_PONPY	Q09242 pongo pygma
21	32	69.6	590	1 PTWA_BACST	P42956 bacillus su
22	32	69.6	639	1 ACW3_CHICK	P49578 gallus gall
23	32	69.6	2139	1 CRB_DROME	P10040 drosophila
24	31	67.4	111	1 PHNA_ECOLI	P16680 escherichia
25	31	67.4	166	1 ING_CEREAL	P28333 cervus elap
26	31	67.4	315	1 ALDR_BOVIN	P16116 bos taurus
27	31	67.4	315	1 ALDR_PIG	P08076 sus scrofa
28	31	67.4	357	1 CHEB_BACST	Q05522 bacillus su
29	31	67.4	363	1 T1SB_MYCPN	P75767 mycoplasma
30	31	67.4	433	1 Y103_MERTTA	Q57567 methanococc
31	31	67.4	635	1 YB64_PYRHO	O59133 pyrococcus
32	31	67.4	724	1 HMMR_HUMAN	O75330 homo sapien
33	31	67.4	905	1 ZO3_MOUSE	Q09xy1 mus musculus

34	31	67.4	1772	1 MSP1_PLAYO	P13828 plasmodium
35	30	65.2	106	1 YBC8_YEAST	P38202 saccharomyc
36	30	65.2	117	1 RPOZ_LACIA	Q9064 lactococcus
37	30	65.2	172	1 YC37_CVAPA	P48277 cyanophora
38	30	65.2	214	1 YJ82_AQUAE	O67790 aquilex aeo
39	30	65.2	314	1 HCDH_PIG	P00348 sus scrofa
40	30	65.2	397	1 YXX7_CASBL	Q18674 caenorhabdi
41	30	65.2	410	1 APGM_PYRAB	Q9V2M6 pyrococcus
42	30	65.2	411	1 APGM_PYRFU	P58814 pyrococcus
43	30	65.2	412	1 APGM_PYRHO	O57742 pyrococcus
44	30	65.2	485	1 YDE5_SCHPO	Q10439 schizosacch
45	30	65.2	619	1 Y707_MERTH	O26803 methanobact

ALIGNMENTS

RESULT 1
HMMR_MOUSE STANDARD; PRT; 794 AA.
ID HMMR_MOUSE
AC Q00547;
DT 01-OCT-1996 (Rel. 34, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Hyaluronan mediated motility receptor (intracellular hyaluronic acid binding protein) (Receptor for hyaluronan-mediated motility).
GN HMMR OR IHABP OR RHAMM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND SUBCELLULAR LOCATION.
RC TISSUE=Lung;
RX MEDLINE=98264863; Pubmed=9601097;
RA Hotman M., Fieber C., Assmann V., Goettlicher M., Sleeman J., Plug R., Howells N., von Stein O., Ponta H., Herrlich P.;
RT "Identification of IHABP, a 95 kDa intracellular hyaluronate binding protein."
RT J. Cell Sci. 111:1673-1684(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhao Y., Zhang S., Turley E.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 1-183 FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=128/SV;
RX MEDLINE=99107769; Pubmed=9889313;
RA Fieber C., Plug R., Sleeman J., Dall P., Ponta H., Hofmann M.;
RT "Characterization of the murine gene encoding the intracellular hyaluronan receptor IHABP."
RL Gene 226:41-50(1999).
RN [4]
RP SEQUENCE OF 164-794 FROM N.A., AND ALTERNATIVE SPLICING.
RC STRAIN=BALB/c; TISSUE=Fibroblast;
RX MEDLINE=96011639; Pubmed=7590272;
RA Entwistle J., Zhang S., Yang B., Wong C., Li Q., Hall C.L., A.J., Mowat M., Greenberg A.H., Turley E.A.;
RT "Characterization of the murine gene encoding the hyaluronan receptor RHAMM."
RL Gene 163:233-238(1995).
RN [5]
RP SEQUENCE OF 318-794 FROM N.A., AND CHARACTERIZATION.
RC STRAIN=BALB/c;
RX MEDLINE=9229690; Pubmed=1376732;
RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D., Cripps V., Austen L., Nance D.M., Turley E.A.;
RT "Molecular cloning of a novel hyaluronan receptor that mediates tumor cell motility."
RL J. Cell Biol. 117:1343-1350(1992).
RN [6]
RP CHARACTERIZATION.
RX MEDLINE=94308286; Pubmed=7518470;

RA Hall C.L., Wang C., Lange L.A., Turley E.A.;
 RT "Hyaluronan and the hyaluronan receptor RHAMM promote focal adhesion
 RT turnover and transient tyrosine kinase activity."; *J. Cell Biol.* 126:575-588 (1994).
 RL J. Cell Biol. 126:575-588 (1994).
 RN [7]
 RP ERK REGULATION AND SUBCELLULAR LOCATION.
 RA MEDLINE=98252222; PubMed=9556628;
 RX Zhang S., Chang M.C., Zyika D., Turley S., Harrison R., Turley E.A.;
 RT "The hyaluronan receptor RHAMM regulates extracellular-regulated
 RT kinase."; *J. Biol. Chem.* 273:11342-11348 (1998).
 RL J. Biol. Chem. 273:11342-11348 (1998).
 RN [8]
 RP REVIEW.
 RA MEDLINE=99059494; PubMed=9845361;
 RX Hofmann M., Asemann V., Fieber C., Sleeman J.P., Moll J., Ponta H.,
 RA Hart I.R., Herrlich P.;
 RT "Problems with RHAMM: a new link between surface adhesion and
 RT oncogenesis?"; *Cell* 95:1591-1592 (1998).
 RL Cell 95:1591-1592 (1998).
 CC -1- FUNCTION: INVOLVED IN CELL MOTILITY. WHEN HYALURONAN BINDS TO
 CC HMMR, THE PHOSPHORYLATION OF A NUMBER OF PROTEINS, INCLUDING THE
 CC FOCAL ADHESION KINASE OCCURS. MAY ALSO BE INVOLVED IN CELLULAR
 CC TRANSFORMATION AND METASTASIS FORMATION, AND IN REGULATING
 CC EXTRACELLULAR-REGULATED KINASE (ERK) ACTIVITY.
 CC -1- SUBUNIT: SUBUNIT OF THE HARC COMPLEX.
 CC -1- ALTERNATIVE PRODUCTS: 2 ISOFORMS; RHAMM1V4 (SHOWN HERE) AND
 CC RHAMM1; ARE PRODUCED BY ALTERNATIVE SPLICING.
 CC -1- TISSUE SPECIFICITY: UBICITOUSLY EXPRESSED.
 CC -----
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 CC -----
 CC EMBL AF031932; AAC12655.1; -;
 DR EMBL AF079222; AAD06670.1; -;
 DR EMBL AJ005919; AAD06676.1; -;
 DR EMBL AJ005920; CA06768.1; JOINED.
 DR EMBL AJ005921; CA06768.1; JOINED.
 DR EMBL AJ005922; CA06768.1; JOINED.
 DR EMBL AJ005923; CA06768.1; JOINED.
 DR EMBL AJ005924; CA06768.1; JOINED.
 DR EMBL X64550; CA045849.1; -;
 DR EMBL X64550; CA045848.1; -;
 DR MGI:104667; Hmnr.
 KW Hyaluronic acid; Alternative splicing; Repeat; Glycoprotein.
 FT DOMAIN 442 546
 FT REPEAT 442 483
 FT REPEAT 463 483
 FT REPEAT 484 504
 FT REPEAT 505 525
 FT REPEAT 526 546
 FT DOMAIN 719 729
 FT DOMAIN 741 750
 FT CARBOHYD 53 53
 FT CARBOHYD 134 134
 FT CARBOHYD 279 279
 FT CARBOHYD 446 446
 FT CARBOHYD 467 467
 FT CARBOHYD 488 488
 FT CARBOHYD 509 509
 FT CARBOHYD 530 530
 FT CARBOHYD 561 561
 FT CARBOHYD 601 601
 FT VARSPIC 218 242
 FT CONFLICT 19 19
 FT CONFLICT 55 55
 FT CONFLICT 71 71
 FT CONFLICT 89 91
 ERE -> Q (IN REF. 2).
 ERE -> Q (IN REF. 2).
 ERE -> Q (IN REF. 2).

FT CONFLICT 94 94 A -> V (IN REF. 3).
 FT CONFLICT 540 540 S -> T (IN REF. 2).
 FT CONFLICT 668 668 E -> D (IN REF. 2).
 SQ SEQUENCE 794 AA; 91799 MW; 74DB3D236224499C CRC64;
 Query Match
 Best Local Similarity 93.5%; Score 43; DB 1; Length 794;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KXKSQLVKRX 10
 Db 741 KXKSQLVKRX 750
 RESULT 2
 HMMR RAT
 ID HMMR RAT STANDARD; PRT; 498 AA.
 AC P97779;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Hyaluronan mediated motility receptor (intracellular hyaluronan acid
 DE binding protein) (Receptor for hyaluronan-mediated motility).
 GN HMMR OR IHABP OR RHAMM.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Vascular smooth muscle;
 RA Savani R.C., Hou G.;
 RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: INVOLVED IN CELL MOTILITY. WHEN HYALURONAN BINDS TO
 CC HMMR, THE PHOSPHORYLATION OF A NUMBER OF PROTEINS, INCLUDING THE
 CC FOCAL ADHESION KINASE OCCURS. MAY ALSO BE INVOLVED IN CELLULAR
 CC TRANSFORMATION AND METASTASIS FORMATION, AND IN REGULATING
 CC EXTRACELLULAR-REGULATED KINASE (ERK) ACTIVITY (BY SIMILARITY).
 CC -1- SUBUNIT: SUBUNIT OF THE HARC COMPLEX.
 CC -1- SUBCELLULAR LOCATION: CELL SURFACE AND CYTOPLASMIC (BY
 CC SIMILARITY).
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL U87983; AAB47997.1; -;
 DR EMBL U87983; AAB47997.1; -;
 KW Hyaluronic acid; Repeat; Glycoprotein.
 FT DOMAIN 420 430
 FT DOMAIN 442 451
 FT CARBOHYD 262 262
 FT CARBOHYD 302 302
 FT CARBOHYD 483 483
 FT CARBOHYD 498 498
 FT SEQUENCE 498 AA; 57858 MW; 58037C79BD5C2A70 CRC64;
 Query Match
 Best Local Similarity 84.8%; Score 39; DB 1; Length 498;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KXKSQLVKRX 10
 Db 442 KXKSQLVKRX 451
 RESULT 3
 ALDR MOUSE
 ID ALDR MOUSE STANDARD; PRT; 315 AA.
 AC P4576;
 DT 01-NOV-1995 (Rel. 32, Created)

DT 01-FEB-1996 (Rel. 33, last sequence update)
 DT 15-JUN-2002 (Rel. 41, last annotation update)
 DE Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase).
 GN AKR1B1 OR ALDRI OR ALDRI1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Kidney;
 RX MEDLINE=95154325; PubMed=7851421;
 RA Gui T., Tanihito T., Kokai Y., Nishimura C.;
 RT "Presence of a closely related subgroup in the aldo-ketoreductase
 family of the mouse."
 RL Eur. J. Biochem. 227:448-453 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR Swiss; TISSUE=Liver;
 RA Iwata T., Carper D.;
 RT Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Kidney;
 RA Daoudal S., Berger M., Pailhoux E., Tournaire C., Veyssiere G.,
 Jean C.;
 RT Submitted (JUN-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: CATALYZES THE NADPH-DEPENDENT REDUCTION OF A WIDE
 VARIETY OF CARBONYL-CONTAINING COMPOUNDS TO THEIR CORRESPONDING
 ALCOHOLS WITH A BROAD RANGE OF CATALYTIC EFFICIENCIES.
 CC -1- CATALYTIC ACTIVITY: Alditol + NAD(P) (+) = aldose + NAD(P)H.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- TISSUE SPECIFICITY: ABUNDANT IN THE TESTIS, SKELETAL MUSCLE AND
 KIDNEY.
 CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: D32250; BAA06980.1; -;
 DR EMBL: U39795; AAB62176.1; -;
 DR EMBL: U29152; AAB69958.1; -;
 DR HSSP: P15121; ZACQ.
 DR SWISS-2DPAGE: P45376; M0USE.
 DR PMMA-2DPAGE: P45376; -;
 DR MGD: MGI:1351494; AKR1b1.
 DR InterPro: IPR001395; Aldo/ket_red.
 DR Pfam: PF00248; Aldo_ket_red.1.
 DR PRINTS: PR00069; ALDKETREDTASE.
 DR ProDom: PD000288; Aldo/ket_red.1.
 DR PROSITE: PS00062; ALDOKETO_REDUCTASE_2; 1.
 DR PROSITE: PS00063; ALDOKETO_REDUCTASE_3; 1.
 DR PROSITE: PS00798; ALDOKETO_REDUCTASE_1; 1.
 DR PROSITE: PS00798; ALDOKETO_REDUCTASE_1; 1.
 DR Oxidoreductase; NADP; Acetylation; Multigene family.
 DR Oxidoreductase; NADP; Acetylation; Multigene family.
 FT INT MET 0
 FT MOD RES 1
 FT ACT SITE 48 48 ACETYLATION (BY SIMILARITY).
 FT CONFLICT 45 45 A -> S (IN REF. 1).
 FT SEQUENCE 315 AA; 35601 MW; 607B604FF432580E CRC64;
 SQ
 Query Match 76.1%; Score 35; DB 1; Length 315;
 Best Local Similarity 70.0%; Pred. No. 8.9;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KKSQLVKRX 10
 DB 61 KLRQVVKRQ 70

RESULT 4
 ALDR_RABIT STANDARD; PRT; 315 AA.
 AC P15122;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-OCT-1996 (Rel. 34, last sequence update)
 DE 15-JUN-2002 (Rel. 41, last annotation update)
 DE Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase).
 GN AKR1B1.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 OX NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=95024191; PubMed=7938022;
 RA Ferraris J.D., Williams C.K., Martin B.M., Burg M.B., Garcia-Perez A.;
 RT "Cloning, genomic organization, and osmotic response of the aldose
 reductase gene."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:10742-10746 (1994).
 RN [2]
 RP SEQUENCE OF 14-315 FROM N.A.
 RC TISSUE=Kidney;
 RX MEDLINE=89380313; PubMed=2506183;
 RA Garcia-Perez A., Martin B., Murphy H.R., Uchida S., Murer H.,
 Cowley B.D. Jr., Handler J.S., Burg M.B.;
 RT "Molecular cloning of cDNA coding for kidney aldose reductase.
 Regulation of specific mRNA accumulation by NaCl-mediated osmotic
 stress."
 RL J. Biol. Chem. 264:16815-16821 (1989).
 CC -1- FUNCTION: CATALYZES THE NADPH-DEPENDENT REDUCTION OF A WIDE
 VARIETY OF CARBONYL-CONTAINING COMPOUNDS TO THEIR CORRESPONDING
 ALCOHOLS WITH A BROAD RANGE OF CATALYTIC EFFICIENCIES.
 CC -1- CATALYTIC ACTIVITY: Alditol + NAD(P) (+) = aldose + NAD(P)H.
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: U13694; AAB60687.1; JOINED.
 DR EMBL: U13689; AAB60687.1; JOINED.
 DR EMBL: U13690; AAB60687.1; JOINED.
 DR EMBL: U13691; AAB60687.1; JOINED.
 DR EMBL: U13692; AAB60687.1; JOINED.
 DR EMBL: U13693; AAB60687.1; JOINED.
 DR EMBL: M32818; AAA31160.1; -;
 DR EMBL: U12316; AAA50833.1; -;
 DR EMBL: J05048; AAA31157.1; -;
 DR PIR: A34406; A34406.
 DR HSSP: P15121; ZACQ.
 DR InterPro: IPR001395; Aldo/ket_red.
 DR Pfam: PF00248; Aldo_ket_red.1.
 DR PRINTS: PR00069; ALDKETREDTASE.
 DR ProDom: PD000288; Aldo/ket_red.1.
 DR PROSITE: PS00062; ALDOKETO_REDUCTASE_2; 1.
 DR PROSITE: PS00063; ALDOKETO_REDUCTASE_3; 1.
 DR PROSITE: PS00798; ALDOKETO_REDUCTASE_1; 1.
 DR Oxidoreductase; NADP; Acetylation.
 FT INT MET 0
 FT MOD RES 1
 FT ACT SITE 48 48 ACETYLATION (BY SIMILARITY).
 FT CONFLICT 45 45 A -> S (IN REF. 1).
 FT SEQUENCE 315 AA; 35632 MW; 64D53B6AC0853FFB CRC64;
 SQ

Query Match 76.1%; Score 35; DB 1; Length 315;
 Best Local Similarity 70.0%; Pred. No. 8.9;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 1 KXKSOVYKRR 10
 61 KXKSOVYKRR 70

RESULT 5
 ALDR RAT STANDARD; PRT; 315 AA.
 ID_P07943;
 AC 01-AUG-1988 (Rel. 08, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Aldose reductase (EC 1.1.1.21) (AR) (Aldohyde reductase).
 GN AKR1B1 OR ALDR1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_Taxid=10116;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN=Sprague-Dawley; TISSUE=Lens;
 RX MEDLINE=87276556; PubMed=3111886;
 RA Carper D., Nishimura C., Shinohara T., Dietzchold B., Wistow G.,
 RA Craft C., Kador P., Kinoshita J.H.;
 RT "Aldose reductase and p-crystallin belong to the same protein
 superfamily as aldehyde reductase.";
 RL FEBS Lett. 220:209-213 (1987).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92084118; PubMed=1748296;
 RA Graham C.E., Szpirer C., Leyan G., Carper D.;
 RT "Characterization of the aldose reductase-encoding gene family in
 rat.";
 RL Gene 107:259-267 (1991).
 RN [3]
 RP SEQUENCE OF 155-168 AND 204-209.
 RC TISSUE=astrocytes;
 RX MEDLINE=96007949; PubMed=7498172;
 RA Laeng P., Boulillon P., Jaupnot L., Labourdette G.;
 RT "Long-term induction of an aldose reductase protein by basic
 fibroblast growth factor in rat astrocytes in vitro.";
 RL Electrophoresis 16:1240-1250 (1995).
 CC -1- FUNCTION: CATALYZES THE NADPH-DEPENDENT REDUCTION OF A WIDE
 VARIETY OF CARBOXYL-CONTAINING COMPOUNDS TO THEIR CORRESPONDING
 ALCOHOLS WITH A BROAD RANGE OF CATALYTIC EFFICIENCIES.
 CC -1- CATALYTIC ACTIVITY: Alditol + NAD(P)(+) = aldose + NAD(P)H.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DISBASE: IN DIABETES AND GALACTOSEMIA, INCREASED AR ACTIVITY LEADS
 TO HIGH LEVELS OF SORBITOL AND GALACTITOL, RESPECTIVELY, IN THE
 CELLS OF MANY TISSUES. ACCUMULATION OF SUGAR ALCOHOLS HAS BEEN
 SHOWN TO CAUSE OSMOTIC CATARACTS IN THE LENS. AR IS ALSO THOUGHT
 TO PLAY A KEY ROLE IN DIABETIC COMPLICATIONS OF THREE OTHER TARGET
 TISSUES, NAMELY, NERVE, KIDNEY AND RETINA.
 CC -1- SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
 CC -----
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 CC -----
 CC EMBL, X05884; AAA29308.1; -
 CC EMBL, M60322; AAA40721.1; -
 CC PIR: S00079; S00079.
 CC HSSP, P15121; ZACO.
 CC InterPro: IPR001395; Aldo/ket_red.

DR Pfam; PF00248; aldo_ket_red; 1.
 DR PRINTS; PR00069; ALDKETREDTASE.
 DR ProDom; PD000288; Aldo/ket_red; 1.
 DR PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
 DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; 1.
 DR PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
 KW Oxidoreductase; NADP; Acetylation.
 FT INIT MET 0
 FT MOD RES 1
 FT ACT SITE 48
 FT SEQUENCE 315 AA; 35666 MW; 572941A154BC1202 CRC64;
 BY SIMILARITY.
 ACETYLATION (BY SIMILARITY).
 HYDROGEN-BOND DONOR (BY SIMILARITY).

Query Match 76.1%; Score 35; DB 1; Length 315;
 Best Local Similarity 70.0%; Pred. No. 8.9;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 1 KXKSOVYKRR 10
 61 KXKSOVYKRR 70

RESULT 6
 POL1 HUMAN STANDARD; PRT; 874 AA.
 ID_P10266; Q14273;
 AC 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Endogenous retrovirus HERV-K10 putative pol polyprotein [includes:
 DE Reverse transcriptase (EC 2.7.7.49); Endonuclease].
 GN POL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=87036922; PubMed=3021993;
 RA Ono M., Yasunaga T., Miyata T., Uehikubo H.;
 RT "Nucleotide sequence of human endogenous retrovirus genome related to
 the mouse mammary tumor virus genome.";
 RL J. Virol. 60:589-598 (1986).
 CC -1- CATALYTIC ACTIVITY: N deoxynucleoside triphosphate = N diphosphate
 + [dNA](n).
 CC -----
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 CC -----
 CC EMBL, M14123; AA88033.1; ALT_SEQ.
 CC PIR: D24483; GNHUR.
 CC InterPro: IPR001037; Integrase_C.
 CC InterPro: IPR003308; Integrase_Zn.
 CC InterPro: IPR002156; RNaseH.
 CC InterPro: IPR00477; RYase.
 CC InterPro: IPR001584; Rve.
 CC Pfam; PF00075; RNaseH; 1.
 CC Pfam; PF00078; RYc; 1.
 CC Pfam; PF00552; Integrase; 1.
 CC Pfam; PF00665; Rve; 1.
 CC Pfam; PF02022; Integrase_Zn; 1.
 KW Hypothetical protein; Hydrolase; Transferase;
 KW RNA-directed DNA polymerase; Nuclease; Endonuclease; Polyprotein.
 FT DOMAIN 36 250
 FT DOMAIN 585 764
 FT SEQUENCE 874 AA; 98936 MW; PD98598979801886 CRC64;
 ENDONUCLEASE.
 REVERSEB_TRANSCRIPTASE.
 Query Match 73.9%; Score 34; DB 1; Length 874;
 Best Local Similarity 77.8%; Pred. No. 38;

DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 15-FEB-1999 (Rel. 38, Last annotation update)
 DE Preprotein translocase secY subunit.
 GN SECY
 OS Bacillus licheniformis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NX NCBI_TaxId=1402;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93062802; PubMed=1435726;
 RA Tschander S., Driesen A.J.W., Freudl R.;
 RT "Cloning and molecular characterization of the secY genes from
 RT Bacillus licheniformis and Staphylococcus carnosus: comparative
 RT analysis of nine members of the SecY family.";
 RL Mol. Genet. 235:147-152(1992).
 CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH SECA AND SECE
 CC TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE PLASMA MEMBRANE,
 CC BY FORMING PART OF A CHANNEL.
 CC -1- SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECY) THAT
 CC COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
 CC -----
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 CC -----
 CC EMBL: X70087; CAA49692.1; -
 CC PIR: S30116; S30116.
 CC PIR: S34403; S34403.
 CC InterPro: IPR002208; SecY.
 DR Pfam: PF00344; secY, 1.
 DR PRINTS: PR00303; SECYTRNLCASE.
 DR TIGRPFAM: TIGR00967; 3a05018007; 1.
 DR PROSITE: PS00755; SECY_1; 1.
 DR PROSITE: PS00756; SECY_2; 1.
 KW Protein transport; Translocation; Transmembrane.
 FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 18 38 POTENTIAL.
 FT DOMAIN 39 63 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 64 84 POTENTIAL.
 FT DOMAIN 85 115 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 116 136 POTENTIAL.
 FT DOMAIN 137 145 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 146 166 POTENTIAL.
 FT DOMAIN 167 174 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 175 195 POTENTIAL.
 FT DOMAIN 196 213 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 214 234 POTENTIAL.
 FT DOMAIN 235 261 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 262 282 POTENTIAL.
 FT DOMAIN 283 308 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 309 329 POTENTIAL.
 FT DOMAIN 330 368 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 369 389 POTENTIAL.
 FT TRANSMEM 390 410 POTENTIAL.
 FT DOMAIN 411 431 CYTOPLASMIC (POTENTIAL).
 SQ SEQUENCE 431 AA; 46996 MW; 9DA26BB7C8487C0 CRC64;

Query Match 71.7%; Score 33; DB 1; Length 431;
 Best Local Similarity 77.8%; Pred. No. 30;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLSKOLVKR 9
 Db 415 QLESOLVKR 423

RESULT 10
 ID SECY_BACSU STANDARD; PRT; 431 AA.
 AC P16336;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Preprotein translocase secY subunit.
 GN SECY.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 NX NCBI_TaxId=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=90251170; PubMed=2110998;
 RA Suh J.-W., Boylan S.A., Thomas S.M., Dolan K.M., Oliver D.B.,
 RA Price C.W.;
 RT "Isolation of a secY homologue from Bacillus subtilis: evidence for a
 RT common protein export pathway in eubacteria.";
 RL Mol. Microbiol. 4:305-314(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90221911; PubMed=2139212;
 RA Yoshikawa H., Doi R.H.;
 RT "Sequence of the Bacillus subtilis spectinomycin resistance gene
 RT region.";
 RL Nucleic Acids Res. 18:1647-1647(1990).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90292990; PubMed=2113521;
 RA Nakamura K., Nakamura A., Takamatsu H., Yoshikawa H., Yamane K.;
 RT "Cloning and characterization of a Bacillus subtilis gene homologous
 RT to E. coli secY.";
 RL J. Biochem. 107:603-607(1990).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96186897; PubMed=8635744;
 RA Suh J.-W., Boylan S.A., Oh S.H., Price C.W.;
 RT "Genetic and transcriptional organization of the Bacillus subtilis
 RT spc-alpha region.";
 RL Gene 169:17-23(1996).
 CC -1- FUNCTION: INVOLVED IN PROTEIN EXPORT. INTERACTS WITH SECA AND SECE
 CC TO ALLOW THE TRANSLOCATION OF PROTEINS ACROSS THE PLASMA MEMBRANE,
 CC BY FORMING PART OF A CHANNEL.
 CC -1- SUBUNIT: ONE OF SEVEN SECRETORY PROTEINS (SECA-F & SECY) THAT
 CC COMPRISE THE PROKARYOTIC PROTEIN TRANSLOCATION APPARATUS.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO THE SECY/SEC61-ALPHA FAMILY.
 CC -----
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 CC -----
 CC EMBL: X51329; CAA35712.1; -
 CC EMBL: M31102; AAB59118.1; -
 CC EMBL: D00619; BAA00495.1; ALT_INIT.
 CC EMBL: L47971; AAB06819.1; -
 CC EMBL: Z99104; CAB11912.1; -
 CC PIR: S08629; BMBSY.
 CC PIR: S12683; S12683.
 CC Subtilist; Bg10445; secY.
 DR InterPro: IPR002208; SecY.
 DR Pfam: PF00344; secY, 1.
 DR PRINTS: PR00303; SECYTRNLCASE.
 DR TIGRPFAM: TIGR00967; 3a05018007; 1.
 DR PROSITE: PS00755; SECY_1; 1.
 DR PROSITE: PS00756; SECY_2; 1.
 KW Protein transport; Translocation; Transmembrane; Complete proteome.

```

FT DOMAIN 1 17 CYTOPLASMIC (POTENTIAL).
RT TRANSSEM 18 39 POTENTIAL.
FT DOMAIN 40 58 EXTRACELLULAR (POTENTIAL).
RT TRANSSEM 51 80 POTENTIAL.
FT DOMAIN 81 114 CYTOPLASMIC (POTENTIAL).
RT TRANSSEM 115 132 POTENTIAL.
FT DOMAIN 133 147 EXTRACELLULAR (POTENTIAL).
RT TRANSSEM 148 167 POTENTIAL.
FT DOMAIN 168 173 CYTOPLASMIC (POTENTIAL).
RT TRANSSEM 174 192 POTENTIAL.
FT DOMAIN 193 216 EXTRACELLULAR (POTENTIAL).
RT TRANSSEM 217 234 POTENTIAL.
FT DOMAIN 225 267 CYTOPLASMIC (POTENTIAL).
RT TRANSSEM 268 291 POTENTIAL.
FT DOMAIN 292 309 EXTRACELLULAR (POTENTIAL).
RT TRANSSEM 310 329 POTENTIAL.
FT DOMAIN 330 366 CYTOPLASMIC (POTENTIAL).
RT TRANSSEM 367 386 POTENTIAL.
FT DOMAIN 387 391 EXTRACELLULAR (POTENTIAL).
RT TRANSSEM 392 410 POTENTIAL.
FT DOMAIN 411 431 CYTOPLASMIC (POTENTIAL).
SQ SEQUENCE 431 AA; 47243 MW; 6AB949378D17D8B4 CRC64;

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Query Match 71.7%; Score 33; DB 1; Length 431;
Best Local Similarity 77.8%; Pred. No. 30;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 KLSQVKKR 9
Db 415 QUESOLVKKR 423

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RESULT 11
YP46_YEAST STANDARD; PRT; 455 AA.
ID YP46_YEAST
AC O12080.
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Hypothetical protein YP146C.
GN YP146C OR YP12C OR P2610.
OS Saccharomyces cerevisiae (baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N. A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97103777; PubMed=8948103;
RT Putnelli B., Coster F., Goffeau A.;
RT "The sequence of 55 kb on the left arm of yeast chromosome XVI
RT identifies a small nuclear RNA, a new putative protein kinase and two
RT new putative regulators.";
RL Yeast 12:1483-1492 (1996).
RN [2]
RP SEQUENCE FROM N. A.
RC STRAIN=S288C / AB972;
RX MEDLINE=97313271; PubMed=9169875;
RT Arcujo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RT Bostein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RT Chung B., Churcher C.M., Coster F., Davis K., Davis R.W.,
RT Dietrich F.S., Delius H., Dipolo T., Dubois E., Duesterhoeft A.,
RT Duncan M., Floeth M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RT Hall J., Hebling U., Hermann K., Hilbert H., Hillier L.,
RT Hunnicke-Smith S., Hyman R., Johnston M., Kalman S., Kleene K.,
RT Komp C., Kurd O., Laskard D., Lew H., Lin A., Lin D., Louis E.J.,
RT Marathe R., Messenguy F., Mewes H.-W., Mitispati S., Moestl D.,
RT Mueller-Auer S., Namath A., Neutwich U., Oefner P., Pearson D.,
RT Petel F.X., Pohl T.M., Putnelli D., Schafer M., Scharfe M.,
RT Scherens B., Schramm S., Schroeder M., Sidic A.M., Tettelein H.,
RT Utrera-Razun L.A., Ushinsky S., Vierdeels F., Vissers S., Voss H.,
RT Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnett E.,

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RA Zhong W.W., Zollner A., Vo D.H., Hani J.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL Nature 387:103-105 (1997).
CC -1- SIMILARITY: BELONGS TO THE GLTSCR2 FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U43703; AAB68216.1; -
DR EMBL; X96770; CAA65547.1; -
DR EMBL; Z73502; CAA97850.1; -.
DR SGD; S0006067; YP146C.
KW Hypothetical protein.
FT DOMAIN 273 276 POLY-GLU.
FT DOMAIN 281 293 POLY-GLU.
SQ SEQUENCE 455 AA; 52555 MW; 9B761B0318EPFC8 CRC64;

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Query Match 71.7%; Score 33; DB 1; Length 455;
Best Local Similarity 66.7%; Pred. No. 32;
Matches 6; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

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Qy 2 LKQVKKR 10
Db 71 LKQVKKR 79

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RESULT 12
ALDR_HUMAN STANDARD; PRT; 315 AA.
ID ALDR_HUMAN
AC P15121.Q9BS21;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Aldose reductase (EC 1.1.1.21) (AR) (Aldehyde reductase).
GN AKR1B1 OR ALDR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N. A., AND PARTIAL SEQUENCE.
RX MEDLINE=89255461; PubMed=2498333;
RT Bohren K.W., Bullock B., Wermuth B., Gabbay K.H.;
RT "The aldo-keto reductase superfamily. cDNAs and deduced amino acid
RT sequences of human aldehyde and aldose reductases.";
RL J. Biol. Chem. 264:9547-9551 (1989).
RN [2]
RP SEQUENCE FROM N. A.
RC TISSUE=Fetal;
RX MEDLINE=90045960; PubMed=2510130;
RT Graham A., Hedge P.J., Powell S.J., Riley J., Brown L., Gammack A.,
RT Carey F., Markham A.F.;
RT "Nucleotide sequence of cDNA for human aldose reductase.";
RL Nucleic Acids Res. 17:8368-8368 (1989).
RN [3]
RP SEQUENCE FROM N. A.
RC TISSUE=Placenta;
RX MEDLINE=89359274; PubMed=2504709;
RT Chung S., Lamendola J.;
RT "Cloning and sequence determination of human placental aldose
RT reductase gene.";
RL J. Biol. Chem. 264:14775-14777 (1989).
RN [4]
RP SEQUENCE FROM N. A.
RC TISSUE=Placenta;
RX MEDLINE=90253609; PubMed=2111143;
RT Grundmann U., Bohn H., Obermeier R., Amann E.;
RT "Cloning and prokaryotic expression of a biologically active human

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RT placental aldose reductase.";
 RL DNA Cell Biol. 9:149-157(1990).
 [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90277668; PubMed=2112546;
 RA Nishimura C., Matsumura Y., Kokai Y., Akera T., Carper D., Morjana N.,
 RT Lyons C., Flynn T.G.;
 RL "Cloning and expression of human aldose reductase.";
 J. Biol. Chem. 265:9788-9792(1990).
 [6]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91201333; PubMed=1901857;
 RA Graham A., Brown L., Hedge P.J., Gammack A.U., Markham A.F.;
 RL "Structure of the human aldose reductase gene.";
 J. Biol. Chem. 266:6872-6877(1991).
 [7]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97341182; PubMed=9195951;
 RA Ko B.C.B., Ruepp B., Bohren K.M., Gabbay K.H., Chung S.S.;
 RT "Identification and characterization of multiple osmotic response
 sequences in the human aldose reductase gene.";
 J. Biol. Chem. 272:16431-16437(1997).
 [8]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain, Eye, and Urinary bladder;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 [9]
 RP SEQUENCE OF 243-274.
 RX MEDLINE=89123393; PubMed=2492527;
 RA Morjana N.A., Lyons C., Flynn T.G.;
 RT "Aldose reductase from human psoas muscle. Affinity labeling of an
 active site lysine by pyridoxal 5'-phosphate and pyridoxal
 5'-diphospho-5'-adenosine.";
 J. Biol. Chem. 264:2912-2913(1989).
 [10]
 RP PARTIAL SEQUENCE, AND ACETYLATION.
 RX TISSUE=Muscle;
 RA MEDLINE=94109388; PubMed=8281941;
 RA Jaquinod M., Potier N., Klarskov K., Reymann J.-M., Sorokine O.,
 RT Kieffer S., Barth P., Andriantomanga V., Biellmann J.-F.,
 RA van Dorsselaer A.;
 RT "Sequence of pig lens aldose reductase and electrospray mass
 spectrometry of non-covalent and covalent complexes.";
 Eur. J. Biochem. 218:893-903(1993).
 [11]
 RP X-RAY CRYSTALLOGRAPHY (1.65 ANGSTROMS).
 RX MEDLINE=92320300; PubMed=1621098;
 RA Wilson D.K., Bohren K.M., Gabbay K.H., Quijcho F.A.;
 RT "An unlikely sugar substrate site in the 1.65 A structure of the
 human aldose reductase holoenzyme implicated in diabetic
 complications.";
 Science 257:81-84(1992).
 [12]
 RP X-RAY CRYSTALLOGRAPHY (2.27 ANGSTROMS).
 RX MEDLINE=93077587; PubMed=1447221;
 RA Bortani D.W., Harter T.M., Petrasch J.M.;
 RT "The crystal structure of the aldose reductase.NADPH binary complex.";
 J. Biol. Chem. 267:24841-24847(1992).
 [13]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RX MEDLINE=94052189; PubMed=8234324;
 RA Wilson D.K., Tarle I., Petrasch J.M., Quijcho F.A.;
 RT "Refined 1.8-A structure of human aldose reductase complexed with the
 potent inhibitor zopolrestat.";
 Proc. Natl. Acad. Sci. U.S.A. 90:9847-9851(1993).
 [14]
 RP X-RAY CRYSTALLOGRAPHY (1.8 ANGSTROMS).
 RX MEDLINE=98070237; PubMed=9405046;
 RA Harrison D.H., Bohren K.M., Peteko G.A., Ringe D., Gabbay K.H.;
 RT "The alrestatin double-decker: binding of two inhibitor molecules to
 human aldose reductase reveals a new specificity determinant.";
 Biochemistry 36:16134-16140(1997).

CC -! FUNCTION: CATALYZES THE NADPH-DEPENDENT REDUCTION OF A WIDE
 CC VARIETY OF CARBONYL-CONTAINING COMPOUNDS TO THEIR CORRESPONDING
 CC ALCOHOLS WITH A BROAD RANGE OF CATALYTIC EFFICIENCIES.
 CC -! CATALYTIC ACTIVITY: Alditol + NAD(P)(+) = aldose + NAD(P)H.
 CC -! SUBUNIT: MONOMER.
 CC -! SUBCELLULAR LOCATION: Cytoplasmic.
 CC -! DISEASE: IN DIABETES AND GALACTOSEMIA, INCREASED AR ACTIVITY LEADS
 CC TO HIGH LEVELS OF SORBITOL AND GALACTITOL, RESPECTIVELY, IN THE
 CC CELLS OF MANY TISSUES. ACCUMULATION OF SUGAR ALCOHOLS HAS BEEN
 CC SHOWN TO CAUSE OSMOTIC CATARACTS IN THE LENS. AR IS ALSO THOUGHT
 CC TO PLAY A KEY ROLE IN DIABETIC COMPLICATIONS OF THREE OTHER TARGET
 CC TISSUES, NAMELY NERVE, KIDNEY AND RETINA.
 CC -! SIMILARITY: BELONGS TO THE ALDO/KETO REDUCTASE FAMILY.
 CC -----
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 CC -----
 DR EMBL, X15414; CAA33460.1; -;
 DR EMBL, J04795; AAA51713.1; -;
 DR EMBL, J05017; AAA51714.1; -;
 DR EMBL, M34720; AAA35560.1; -;
 DR EMBL, M34721; AAA35561.1; -;
 DR EMBL, J05474; AAA51715.1; -;
 DR EMBL, M59783; AAA51712.1; -;
 DR EMBL, M59856; AAA51712.1; JOINED.
 DR EMBL, AF032455; AAB88851.1; -;
 DR EMBL, BC000260; AAH00260.1; -;
 DR EMBL, BC005387; AAH05387.1; -;
 DR EMBL, BC010391; AAH010391.1; -;
 DR PIR, S06591; S06591.
 DR PIR, A34583; A34583.
 DR PIR, B33851; B33851.
 DR PIR, A31432; A31432.
 DR PIR, A36436; A36436.
 DR PIR, A36510; A36510.
 DR PIR, A39763; A39763.
 DR PDB, 1ADS; 31-OCT-93.
 DR PDB, 1ABN; 31-JAN-94.
 DR PDB, 2ACQ; 31-JUL-94.
 DR PDB, 2ACR; 31-JUL-94.
 DR PDB, 2ACS; 31-JUL-94.
 DR PDB, 2ACU; 31-JUL-94.
 DR PDB, 1MAR; 20-JUL-95.
 DR PDB, 1AZ1; 18-MAR-98.
 DR PDB, 1AZ2; 18-MAR-98.
 DR Aairnus/Chent-2DPAGE; 1202; IEF.
 DR Genew; HGNC:381; AKR1B1.
 DR MIM; 103880; -;
 DR InterPro; IPR001395; Aldo/ket_red.
 DR Pfam; PF00248; Aldo_ket_red; 1.
 DR PRINTS; PR00069; ALDKETREDTASE.
 DR Prodom; PD000288; Aldo/ket_red; 1.
 DR PROSITE; PS00062; ALDOKETO_REDUCTASE_2; 1.
 DR PROSITE; PS00063; ALDOKETO_REDUCTASE_3; 1.
 DR PROSITE; PS00798; ALDOKETO_REDUCTASE_1; 1.
 KW Oxidoreductase; NADP; Acetylation; 3D-structure.
 FT INIT MET 0
 FT MOD RES 1
 FT NP BIND 9
 FT ACT SITE 48
 FT CONFLICT 4
 FT CONFLICT 141
 FT CONFLICT 269
 FT STRAND 7
 FT TURN 3
 FT STRAND 11
 FT STRAND 13
 FT STRAND 15
 FT STRAND 17

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FT TURN 20 21
FT HELIX 24 37
FT TURN 38 38
FT STRAND 41 43
FT HELIX 46 48
FT TURN 49 49
FT HELIX 51 64
FT TURN 65 65
FT STRAND 69 71
FT STRAND 73 78
FT HELIX 80 82
FT TURN 85 87
FT HELIX 88 99
FT TURN 100 100

Query Match
Best Local Similarity 69.6%; Score 32; DB 1; Length 315;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKSQLVKRR 10
Db 61 KLRGVKRR 70

RESULT 13
ACM3_MOUSE STANDARD; PRT; 589 AA.
ID ACM3_MOUSE
AC 09ERZ3; 064055;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Muscarinic acetylcholine receptor M3 (Mm3 mChR).
GN CHRM3 OR CHRM-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
RN SEQUENCE FROM N.A.
RP Gomeza J., Weiss J.;
RA "Isolation, sequence and functional expression of mouse muscarinic
RT acetylcholine receptor gene."
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 314-439 FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=95179320; PubMed=7874308;
RX Andre C., Dos Santos G., Koulakoff A.;
RA "Cultured neurons from mouse brain reproduce the muscarinic receptor
RT profile of their tissue of origin."
RL Eur. J. Neurosci. 6:1691-1701(1994).
CC -!- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLYLATE CYCLASE,
BREAKDOWN OF PHOSPHOLIPIDS & MODULATION OF POTASSIUM CHANNELS
THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
TURNOVER.
CC -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC -!- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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-----
DR EMBL; AF264050; AAG1344.1; -.
DR EMBL; S74908; AAB33576.2; -.
DR MGD; MGI:88398; Chrm3.
DR InterPro: IPR000276; GPCR_Rhodopsn.
DR Pfam; PF00001; 7tm_1.1.
DR PRINTS; PR00237; GPCRHHODOPSN.

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DR PROSITE; PS00237; G_PROTEIN_RECEP_F1_1; 1.
DR PROSITE; PS50262; G_PROTEIN_RECEP_F1_2; 1.
KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
KW Phosphorylation; Multigene family; G-protein coupled receptor.
FT DOMAIN 1 66
FT TRANSMEM 67 90
FT DOMAIN 91 103
FT TRANSMEM 104 124
FT DOMAIN 125 141
FT TRANSMEM 142 163
FT DOMAIN 164 183
FT TRANSMEM 184 206
FT DOMAIN 207 228
FT TRANSMEM 229 251
FT DOMAIN 252 491
FT TRANSMEM 492 512
FT DOMAIN 513 526
FT TRANSMEM 527 546
FT DOMAIN 547 589
FT CARBOHYD 6 6
FT CARBOHYD 15 15
FT CARBOHYD 41 41
FT CARBOHYD 48 48
FT CARBOHYD 52 52
FT DISULFID 140 220
SQ SEQUENCE 589 AA; 66211 MW; AB782149EBE7804 CRC64;
BY SIMILARITY.

Query Match
Best Local Similarity 69.6%; Score 32; DB 1; Length 589;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KKSQLVKRR 10
Db 469 KTRSQITKRR 478

RESULT 14
ACM3_RAT STANDARD; PRT; 589 AA.
ID ACM3_RAT
AC P08483; 08QWK9;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-NOV-1988 (Rel. 09, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Muscarinic acetylcholine receptor M3.
GN CHRM3 OR CHRM-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE=87263421; PubMed=3037705;
RA Bonner T.I., Buckley N.J., Young A.C., Brann M.R.;
RT "Identification of a family of muscarinic acetylcholine receptor
RL genes."
RN Science 237:527-532(1987).
[2]
RN REVISION TO 184.
RX MEDLINE=90166521; PubMed=3272174;
RA Bonner T.I., Young A.C., Brann M.R., Buckley N.J.;
RT "Cloning and expression of the human and rat m5 muscarinic
RL acetylcholine receptor genes."
RN Neuron 1:403-410(1988).
[3]
RN SEQUENCE FROM N.A.
RP TISSUE=Brain;
RC MEDLINE=88077068; PubMed=3120722;
RX Brann T., Schofield P.R., Shivers B.D., Pritchett D.B., Seeburg P.H.;
RT "A novel subtype of muscarinic receptor identified by homology
RL screening."
RN Biochem. Biophys. Res. Commun. 149:125-132(1987).
[4]
RN SEQUENCE FROM N.A.

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RC TISSUE=iris; MEDLINE=99138467; PubMed=9972520;
 RX Furuta M., Ohya S., Imaizumi Y., Watanabe M.;
 RA "Molecular cloning of m3 muscarinic acetylcholine receptor in rat
 RT iris.";
 RL J. Smooth Muscle Res. 34:111-122(1998).
 RN (5)
 RP MUTAGENESIS.
 RX MEDLINE=92037535; PubMed=1657592;
 RA Wess J., Gubla D., Brann M.R.;
 RT "Site-directed mutagenesis of the m3 muscarinic receptor:
 RT identification of a series of threonine and tyrosine residues
 RT involved in agonist but not antagonist binding.";
 RL EMBO J. 10:3729-3734(1991).
 RN [6]
 RP MUTAGENESIS.
 RX MEDLINE=92406875; PubMed=1527051;
 RA Wess J., Maggic R., Palmer J.R., Vogel Z.;
 RT "Role of conserved threonine and tyrosine residues in acetylcholine
 RT binding and muscarinic receptor activation. A study with m3
 RT muscarinic receptor point mutants.";
 RL J. Biol. Chem. 267:1913-1919(1992).
 CC -1- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
 CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
 CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
 CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
 CC TURNOVER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
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 CC -----
 CC EMBL: M16407; AAA40661.1; ALT_SEQ.
 CC EMBL: M16408; AAA40662.1; ALT_SEQ.
 CC EMBL: M18088; AAA40655.1; -.
 CC EMBL: M62826; AAA41553.1; -.
 CC EMBL: AB017656; BAA36839.1; -.
 CC PIR: B29514; B29514.
 CC PIR: A29476; A29476.
 CC InterPro: IPR000276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm_1, 1.
 DR PROSITE: PRO0237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN RECP_F1_2; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
 KW phosphorylation; Multigene family; G-protein coupled receptor.
 FT DOMAIN 1 66
 FT TRANSMEM 67 90
 FT DOMAIN 91 103
 FT TRANSMEM 104 124
 FT DOMAIN 125 141
 FT TRANSMEM 142 163
 FT DOMAIN 164 183
 FT TRANSMEM 184 206
 FT DOMAIN 207 228
 FT TRANSMEM 229 251
 FT DOMAIN 252 291
 FT TRANSMEM 292 312
 FT DOMAIN 313 326
 FT TRANSMEM 327 346
 FT DOMAIN 347 359
 FT TRANSMEM 360 389
 FT CARBOHYD 15 15
 FT CARBOHYD 41 41
 FT CARBOHYD 48 48
 FT CARBOHYD 52 52
 FT DISULFID 140 220

FT CONFLICT 184 184 A -> R (IN REF. 4).
 FT CONFLICT 516 516 C -> R (IN REF. 3).
 FT CONFLICT 556 556 T -> M (IN REF. 3).
 SQ SEQUENCE 589 AA; 66065 MM; 9A5EF2FA653C930A CXC64;
 Query Match 69.6%; Score 32; DB 1; Length 589;
 Best Local Similarity 60.0%; Pred. No. 66;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KXKSLVKK 10
 Db 469 KTRSQITKK 478
 RESULT 15
 AC M3 BOVIN STANDARD; PRT; 590 AA.
 ID AC M3 BOVIN STANDARD; PRT; 590 AA.
 AC P41984;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE Muscarinic acetylcholine receptor M3.
 GN CHRM3.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RP TISSUE=Brain;
 RX MEDLINE=94339178; PubMed=8061048;
 RT Lee P.H., Hodges P.K., Glickman P., Chang K.J.;
 RT "Cloning and expression of a cDNA encoding bovine muscarinic
 RT acetylcholine m3 receptor.";
 RL Biochim. Biophys. Acta 1223:151-154(1994).
 RN [2]
 RP SEQUENCE OF 327-467 FROM N.A.
 RP TISSUE=Adrenal gland;
 RA Sui A.-L., Chou W.-Y., Kao L.-S.;
 RA Submitted (XXX-1994) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: THE MUSCARINIC ACETYLCHOLINE RECEPTOR MEDIATES VARIOUS
 CC CELLULAR RESPONSES, INCLUDING INHIBITION OF ADENYLATE CYCLASE,
 CC BREAKDOWN OF PHOSPHOINOSITIDES & MODULATION OF POTASSIUM CHANNELS
 CC THROUGH THE ACTION OF G PROTEINS. PRIMARY TRANSDUCING EFFECT IS PI
 CC TURNOVER.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
 CC -----
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 CC -----
 CC EMBL: U08286; AAA51866.1; -.
 CC EMBL: L27103; AAA30653.1; -.
 CC InterPro: IPR00276; GPCR_Rhodopsn.
 CC Pfam: PF00001; 7tm_1, 1.
 DR PROSITE: PRO0237; GPCR_Rhodopsn.
 DR PROSITE: PS00237; G-PROTEIN RECP_F1_1; 1.
 DR PROSITE: PS50262; G-PROTEIN RECP_F1_2; 1.
 KW Postsynaptic membrane; Ionic channel; Glycoprotein; Transmembrane;
 KW phosphorylation; Multigene family; G-protein coupled receptor.
 FT DOMAIN 1 67
 FT TRANSMEM 68 91
 FT DOMAIN 92 104
 FT TRANSMEM 105 125
 FT DOMAIN 126 142
 FT TRANSMEM 143 164
 FT DOMAIN 165 184
 FT TRANSMEM 185 206
 FT DOMAIN 207 228
 FT TRANSMEM 229 251
 FT DOMAIN 252 291
 FT TRANSMEM 292 312
 FT DOMAIN 313 326
 FT TRANSMEM 327 346
 FT DOMAIN 347 359
 FT TRANSMEM 360 389
 FT CARBOHYD 15 15
 FT CARBOHYD 41 41
 FT CARBOHYD 48 48
 FT CARBOHYD 52 52
 FT DISULFID 140 220

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:38:45 ; Search time 22.6667 Seconds
(without alignments)
90.903 Million cell updates/sec

Title: US-09-685-010-31

Perfect score: 46
Sequence: 1 KLSQVLVYRK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	43	93.5	476	11 Q92026	Q92026 mus sp. hya
2	43	93.5	836	11 Q92026	Q92026 mus musculus
3	39	88.8	713	11 Q9WU77	Q9WU77 ratu
4	38	82.6	232	10 Q942A1	Q942A1 oryza sativ
5	38	82.6	235	10 Q9FRZ1	Q9FRZ1 zea mays (m
6	38	82.6	236	10 Q9FRZ0	Q9FRZ0 zea mays (m
7	38	82.6	640	16 Q9CTU9	Q9CTU9 lactococcus
8	37	80.4	93	5 Q95Q71	Q95Q71 caenorhabdi
9	37	80.4	336	5 Q95Q71	Q95Q71 caenorhabdi
10	36	78.3	82	6 Q95JG7	Q95JG7 ovis aries
11	36	78.3	82	6 Q95JG7	Q95JG7 ovis aries
12	35	76.1	68	2 Q98PM2	Q98PM2 bos taurus
13	35	76.1	68	2 Q98PM2	Q98PM2 bos taurus
14	35	76.1	186	2 Q9ZB38	Q9ZB38 ureaplasma
15	35	76.1	198	2 Q9ZB37	Q9ZB37 ureaplasma
16	35	76.1	207	4 Q96N18	Q96N18 homo sapien

17	35	76.1	276	2 Q9Z3D1	Q9Z3D1 ureaplasma
18	35	76.1	277	2 Q9RH88	Q9RH88 ureaplasma
19	35	76.1	282	2 Q9RH89	Q9RH89 ureaplasma
20	35	76.1	282	2 Q9Z356	Q9Z356 ureaplasma
21	35	76.1	283	2 Q9Z3D4	Q9Z3D4 ureaplasma
22	35	76.1	316	3 P78909	P78909 schizosacch
23	35	76.1	316	11 Q70130	Q70130 mus musculu
24	35	76.1	316	11 Q99KC9	Q99KC9 mus musculu
25	35	76.1	341	2 Q93166	Q93166 escherichia
26	35	76.1	456	3 Q94709	Q94709 schizosacch
27	35	76.1	487	2 Q9ZB39	Q9ZB39 ureaplasma
28	35	76.1	601	5 Q9V6M8	Q9V6M8 drosophila
29	35	76.1	601	5 Q9V6M8	Q9V6M8 drosophila
30	34	73.9	34	16 Q50694	Q50694 borrelia bu
31	34	73.9	75	11 Q8R4N5	Q8R4N5 mus musculu
32	34	73.9	137	5 Q9N306	Q9N306 caenorhabdi
33	34	73.9	263	11 Q9QZV1	Q9QZV1 mus musculu
34	34	73.9	306	16 Q9ZDB2	Q9ZDB2 rickettsia
35	34	73.9	522	12 Q9YV70	Q9YV70 melanoplus
36	34	73.9	633	17 Q9V0U0	Q9V0U0 pyrococcus
37	34	73.9	702	4 Q96P15	Q96P15 homo sapien
38	34	73.9	702	15 Q9OC07	Q9OC07 human endog
39	34	73.9	872	15 Q9WTK9	Q9WTK9 human endog
40	34	73.9	872	15 Q9WTK9	Q9WTK9 human endog
41	34	73.9	875	15 Q9WTK9	Q9WTK9 human endog
42	34	73.9	956	4 Q9BXR4	Q9BXR4 homo sapien
43	34	73.9	956	4 Q9BXR3	Q9BXR3 homo sapien
44	34	73.9	956	4 Q9UP31	Q9UP31 homo sapien
45	34	73.9	1653	5 Q9VIT9	Q9VIT9 drosophila
	34	73.9	1755	4 Q9UKH6	Q9UKH6 homo sapien

ALIGNMENTS

RESULT 1

ID Q92026 PRELIMINARY; PRT; 476 AA.
AC Q92026;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hyaluronan receptor.
OS Mus sp.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9229690; PubMed=1376732;
RA Hardwick C., Hoare K., Owens R., Hohn H.P., Hook M., Moore D.,
RT Clippes V., Austen L., Nance D.M., Turley E.A.;
RT "Molecular cloning of a novel hyaluronan receptor that mediates tumor cell motility.";
RT J. Cell Biol. 117:1343-1350(1992).
DR J. Cell Biol. 117:1343-1350(1992).
KW Receptor.
SQ SEQUENCE 476 AA; 55486 MW; 62DCA82045EE0CB2 CRC64;

Query Match 93.5%; Score 43; DB 11; Length 476;
Best Local Similarity 90.0%; Pred. No. 2.4;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLSQVLVYRK 10
DB 423 KLSQVLVYRK 432

RESULT 2

Q9VDR2 PRELIMINARY; PRT; 836 AA.
 AC Q9VDR2;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Similar to hyaluronan mediated motility receptor (RHAMM).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021427; AAH21427.1; -.
 KW Receptor.
 SQ SEQUENCE 836 AA; 96670 MW; B9BDDA22EBCA652 CRC64;

Query Match 93.5%; Score 43; DB 11; Length 836;
 Best Local Similarity 90.0%; Pred. No. 3.9;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLSQVLKRR 10
 ||:|||||
 Db 783 KLSQVLKRR 792

RESULT 3
 Q9WUF7 PRELIMINARY; PRT; 713 AA.
 ID Q9WUF7;
 AC Q9WUF7;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Hyaluronan receptor RHAMM.
 GN RHAMM.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA STRAIN=SPRAGUE DAWLEY;
 RL "X", Lynn B., Nagy J.I., Cattini P.A.;
 RT "RHAMM cDNA from rat brain."
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PHOCHROMOCYTOMA;
 RA Lynn B.D., Li X., Cattini P.A., Nagy J.I.;
 RT "Sequence, protein expression and erk association of the hyaladherin
 RT RHAMM in PC12 cells."
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF133037; AAD24473.1; -.
 DR EMBL; AF336825; AAK21904.1; -.
 KW Receptor.
 SQ SEQUENCE 713 AA; 82395 MW; 2FE310D5759C6CB3 CRC64;

Query Match 84.8%; Score 39; DB 11; Length 713;
 Best Local Similarity 80.0%; Pred. No. 21;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLSQVLKRR 10
 ||:|||||
 Db 657 KLSQVLKRR 666

RESULT 4
 Q942A1

ID Q942A1 PRELIMINARY; PRT; 232 AA.
 AC Q942A1;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Putative response regulator.
 GN P0431G06.8.
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriocaridaceae; Oryzaceae; Oryza.
 OX NCBI_TaxID=4530;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. NIPPONBARE;
 RA Sasaki T., Matsunoto T., Yamamoto K.;
 RT "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, PAC
 RT clone:P0431G06."
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AP003683; BAB64697.1; -.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF00072; Response_reg.1.
 DR ProDom: PD000039; Response_reg.1.
 KW Phosphorylation; Sensory transduction.
 SQ SEQUENCE 232 AA; 24863 MW; 5454CA63CF2EF95D CRC64;

Query Match 82.6%; Score 38; DB 10; Length 232;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLSQVLKRR 10
 |||||:||||
 Db 141 KLSQVLKRR 150

RESULT 5
 Q9FRZ1 PRELIMINARY; PRT; 235 AA.
 ID Q9FRZ1;
 AC Q9FRZ1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Response regulator 4.
 GN ZMR4.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoidae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GOLDEN CROSS BANTAM T51;
 RA Sakibara H., Sugiyama T.;
 RT "Cloning and characterization of maize response regulators."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB042261; BAB20579.1; -.
 DR InterPro: IPR001789; Response_reg.
 DR Pfam: PF00072; Response_reg.1.
 DR ProDom: PD000039; Response_reg.1.
 DR SMART: SM00448; REC; 1.
 KW Phosphorylation; Sensory transduction.
 SQ SEQUENCE 235 AA; 25664 MW; A53C205400141DCE CRC64;

Query Match 82.6%; Score 38; DB 10; Length 235;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLSQVLKRR 10
 |||||:||||
 Db 148 KLSQVLKRR 157

RESULT 6

Q9FRZ0 PRELIMINARY; PRT; 236 AA.
 ID Q9FRZ0;
 AC Q9FRZ0;
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Response regulator 5.
 GN ZMRK5.
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 OC Panicoideae; Andropogoneae; Zea.
 OK NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. GOLDEN CROSS BANTAM T51;
 RA Sakakibara H., Sugiyama T.;
 RT "Cloning and characterization of maize response regulators."
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB042267; BAB20580.1; -.
 DR InterPro; IPR001789; Response_reg.
 DR Pfam; PF00072; response_reg.1.
 DR ProDom; PD000039; Response_reg.1.
 DR SMART; SM00448; REC; 1.
 DR Phosphorylation; Sensory transduction.
 KW SEQUENCE 236 AA; 25454 MW; 5F8CEC49AFF31D4E CRC64;

Query Match 82.6%; Score 38; DB 10; Length 236;
 Best Local Similarity 80.0%; Pred. No. 12;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KXKSQVKKR 10
 |||||:
 DB 136 KXKSHLKKR 145

RESULT 7
 ID Q9CIU9 PRELIMINARY; PRT; 640 AA.
 AC Q9CIU9;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Fructose-1,6-bisphosphatase (EC 3.1.3.11).
 GN FBP OR IL0257.
 OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
 OC Streptococcaceae; Lactococcus.
 OK NCBI_TaxID=1360;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=IL1403;
 RX MEDLINE=21235186; PubMed=11337471;
 RA Bolotin A., Wincker P., Manger S., Jallion O., Malarme K.,
 RA Weisenbach J., Ehrlich S.D., Sorokin A.;
 RT "The complete genome sequence of the lactic acid bacterium Lactococcus
 RT lactis ssp. lactis IL1403."
 RL Genome Res. 11:731-753(2001).
 DR EMBL; AE006263; AAK04355.1; -.
 KW Complete proteome.
 SQ SEQUENCE 640 AA; 73845 MW; 509CF962273A3BCE CRC64;

Query Match 82.6%; Score 38; DB 16; Length 640;
 Best Local Similarity 70.0%; Pred. No. 29;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXKSQVKKR 10
 |||||:
 DB 311 KXKSQVKKR 320

RESULT 8
 Q95Q71

ID Q95Q71 PRELIMINARY; PRT; 93 AA.
 AC Q95Q71;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 10.5 kDa protein.
 GN C37A2.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderiinae; Caenorhabditis.
 OK NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Le T.T., Kemp K., Scheet P.;
 RT "The sequence of C. elegans cosmid C37A2."
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission."
 RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U97194; AL02460.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 93 AA; 10511 MW; BA4742BB9C94F8A5 CRC64;

Query Match 80.4%; Score 37; DB 5; Length 93;
 Best Local Similarity 70.0%; Pred. No. 8.3;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXKSQVKKR 10
 |||||:
 DB 48 KXKSHLKKR 57

RESULT 9
 ID Q01506 PRELIMINARY; PRT; 336 AA.
 AC Q01506;
 DT 01-JUL-1997 (TREMBlrel. 04, Created)
 DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Hypothetical 39.7 kDa protein.
 GN C37A2.8.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderiinae; Caenorhabditis.
 OK NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BRISTOL N2;
 RA Le T.T., Kemp K., Scheet P.;
 RT "The sequence of C. elegans cosmid C37A2."
 RL Submitted (Apr-1997) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RC STRAIN=BRISTOL N2;
 RA Waterston R.;
 RL "Direct Submission."
 DR EMBL, U07194; AAB52452.1; -.
 KW Hypothetical protein.
 SQ SEQUENCE 336 AA; 39659 MW; BC0322EB7734294 CRC64;

Query Match
 Best Local Similarity 70.0%; Score 37; DB 5; Length 336;
 Matches 7; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 KLSQVLVKKR 10
 DB 48 KLRQLTKRK 57

RESULT 10

O95JG7 PRELIMINARY; PRT; 82 AA.
 AC O95JG7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DE Hyaluronic acid-mediated motility receptor (Fragment).
 OS Ovis aries (Sheep).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Caprinae; Ovis.
 NC NCB1_TaxID=9940;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=TRACHEA;
 RA Aoki T.A., Foreza R.N., Conner G.B.;

RT "Receptor for hyaluronic acid mediated motility in sheep (Ovis aries)
 RL trachea." (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF310973; AAK69578.1; -.
 KW Receptor.
 FT NON_TER 1 1
 FT SEQUENCE 82 AA; 9452 MW; 46B87555C0F1B66 CRC64;

Query Match
 Best Local Similarity 70.0%; Score 36; DB 6; Length 82;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KLSQVLVKKR 10
 DB 50 KLRQLTKRK 59

RESULT 11

O8SPM2 PRELIMINARY; PRT; 82 AA.
 AC O8SPM2;
 DT 01-JUN-2002 (TREMBLrel. 21, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Receptor for hyaluronic acid mediated motility (Fragment).
 GN RHAMN.

OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovine; Bos.
 NC NCB1_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.

RC TISSUE=OVARY;
 RA Schoenfelder M., Einspanier R.;

RT "Expression of HAS-system during oocyte maturation in the cow.";
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, A439694; CAD29126.1; -.

FT NON_TER 1 1
 FT NON_TER 82 82
 SQ SEQUENCE 82 AA; 9452 MW; 46B87555C0F1B66 CRC64;

Query Match
 Best Local Similarity 70.0%; Score 36; DB 6; Length 82;
 Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KLSQVLVKKR 10
 DB 50 KLRQLTKRK 59

RESULT 12

O9S689 PRELIMINARY; PRT; 68 AA.
 AC O9S689;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Multiple banded antigen (Fragment).
 GN MBA.

OS Ureaplasma urealyticum (Ureaplasma urealyticum biotype 2).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Ureaplasma.
 NC NCB1_TaxID=2130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MBA TYPE 8;
 RX MEDLINE=98411422; PubMed=9738062;
 RA Knox C.L., Timms P.;

RT "Comparison of PCR, nested PCR, and random amplified polymorphic DNA
 RT PCR for detection and typing of Ureaplasma urealyticum in specimens
 RT from pregnant women.";
 RL J. Clin. Microbiol. 36:3032-3039 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MBA TYPE 8;
 RX MEDLINE=99045873; PubMed=9828433;
 RA Knox C.L., Giffard P., Timms P.;

RT "The phylogeny of Ureaplasma urealyticum based on the mba gene
 RT fragment."
 RL Int. J. Syst. Bacteriol. 48:1323-1331 (1998).
 DR EMBL, AF108876; AAD19955.1; -.
 FT NON_TER 68 68
 FT SEQUENCE 68 AA; 7403 MW; F67249C2863P6991 CRC64;

OY 1 KLSQVLVKKR 10
 DB 38 KLSQVLVKKR 47

RESULT 13

O9Z607 PRELIMINARY; PRT; 68 AA.
 AC O9Z607;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Multiple banded antigen (Fragment).
 GN MBA.

OS Ureaplasma urealyticum (Ureaplasma urealyticum biotype 2).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Ureaplasma.
 NC NCB1_TaxID=2130;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=MBA TYPE X;
 MEDLINE=98411422; PubMed=9738062;

RA Knox C.L., Timms P.;
 RT "Comparison of PCR, nested PCR, and random amplified polymorphic DNA
 RT PCR for detection and typing of Ureaplasma urealyticum in specimens
 RT from pregnant women.";
 RL J. Clin. Microbiol. 36:3032-3039 (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MBA TYPE X;
 RA MEDLINE=99045873; PubMed=9828433;
 RA Knox C.L., Giffard P., Timms P.;
 RT "The phylogeny of Ureaplasma urealyticum based on the mba gene
 RT fragment.";
 RL Inc. J. Syst. Bacteriol. 48:1323-1331 (1998).
 DR EMBL; AF108877; AAD19956.1; -.
 FT NON TER 68
 SQ SEQUENCE 68 AA; 7416 MW; F71049D5663D6993 CRC64;

Query Match 76.1%; Score 35; DB 2; Length 68;
 Best Local Similarity 80.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIKSQLYKRX 10
 DB 38 KISSQLYKSK 47

RESULT 14
 Q9ZB38 PRELIMINARY; PRT; 186 AA.
 AC Q9ZB38;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
 DE Multiple banded antigen (Fragment).
 OS Ureaplasma urealyticum (Ureaplasma urealyticum biotype 2).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Ureaplasma.
 OC NCBI_TaxID=2130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zheng X., Teng L.-J., Watson H.L., Glass J.I., Cassell G.H.;
 RT "Sequence analysis of the major serovar specific antigen (MB antigen)
 RT genes from different serovars of Ureaplasma urealyticum.";
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50460; AAD00076.1; -.
 FT NON TER 186
 SQ SEQUENCE 186 AA; 19875 MW; AFD6E3BB8F504DC CRC64;

Query Match 76.1%; Score 35; DB 2; Length 186;
 Best Local Similarity 80.0%; Pred. No. 38;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIKSQLYKRX 10
 DB 38 KISSQLYKSK 47

RESULT 15
 Q9ZB37 PRELIMINARY; PRT; 198 AA.
 AC Q9ZB37;
 DT 01-MAY-1999 (TrEMBLrel. 10, Created)
 DT 01-MAY-1999 (TrEMBLrel. 10, last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, last annotation update)
 DE Multiple banded antigen (Fragment).
 OS Ureaplasma urealyticum (Ureaplasma urealyticum biotype 2).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
 OC Mycoplasmataceae; Ureaplasma.
 OC NCBI_TaxID=2130;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zheng X., Teng L.-J., Watson H.L., Glass J.I., Cassell G.H.;
 RT "Sequence analysis of the major serovar specific antigen (MB antigen)

RT genes from different serovars of Ureaplasma urealyticum.";
 RL Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U50461; AAD00077.1; -.
 FT NON TER 198
 SQ SEQUENCE 198 AA; 21212 MW; F0E1DEE5741FA168 CRC64;

Query Match 76.1%; Score 35; DB 2; Length 198;
 Best Local Similarity 80.0%; Pred. No. 40;
 Matches 8; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 KIKSQLYKRX 10
 DB 38 KISSQLYKSK 47

Search completed: February 8, 2003, 10:42:44
 Job time : 23.6667 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:35:55 ; Search time 29 Seconds
(without alignments)
45,948 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KLSQLVKK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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23: /SID2/gcgdata/geneSeq/geneSeq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	100.0	10	23	ABG60827	Hyaluronan (HA) b
2	43	93.5	10	14	AAK6551	Hyaluronan recepto
3	43	93.5	10	18	AAW59164	Mouse RHAMM bindin
4	43	93.5	11	23	ABG60822	Cellular response
5	43	93.5	32	17	AAK99677	Hyaluronan binding
6	43	93.5	32	23	ABG60846	Receptor for hyala
7	43	93.5	476	14	AAK43563	Hyaluronan recepto
8	43	93.5	606	17	AAK99673	Receptor for hyalu
9	43	93.5	630	17	AAW59166	Mouse RHAMM protei
10	43	93.5	631	18	AAK99675	RHAMM 1-2a isoform

11	43	93.5	631	23	ABG60843	Mouse receptor for
12	43	93.5	794	23	AAU11437	Mouse hyaluronin a
13	39	84.8	10	18	AAW59168	Rat RHAMM binding
14	39	84.8	713	23	AAU11438	Rat hyaluronin aci
15	38	82.6	9	14	AAK46550	Hyaluronan recepto
16	38	82.6	9	23	ABG60850	Cellular response
17	38	82.6	10	23	AAU11442	Hyaluronin acid-bl
18	38	82.6	216	22	ABK48053	Signal transductio
19	38	82.6	640	23	ABK53563	Lactococcus lactis
20	35	76.1	316	19	AAW69357	Rat lens aldose re
21	35	76.1	316	23	ABK83356	Murine TSAP6 bindi
22	35	76.1	601	22	ABK60907	Drosophila melanog
23	34	73.9	188	22	AAU69871	Human prostate CDN
24	34	73.9	188	22	AAW01226	Human prostate-spe
25	34	73.9	188	23	ABK59331	Human P1020C prote
26	34	73.9	422	23	AAE24061	Human prostate spe
27	34	73.9	633	22	AAK96656	Putative P. abyssi
28	34	73.9	1119	22	ABG19122	Novel human diago
29	34	73.9	1124	22	ABG19125	Novel human diago
30	34	73.9	1141	22	ABG00388	Novel human diago
31	34	73.9	1396	22	ABG12563	Novel human diago
32	34	73.9	1465	22	ABG00387	Novel human diago
33	34	73.9	1489	22	ABG19124	Novel human diago
34	34	73.9	1490	22	ABG19123	Novel human diago
35	34	73.9	1653	22	ABK71860	Drosophila melanog
36	34	73.9	1883	22	ABG19121	Novel human diago
37	34	73.9	1909	22	ABG19127	Novel human diago
38	34	73.9	2002	22	ABG12556	Novel human diago
39	34	73.9	2383	22	ABG00402	Novel human diago
40	33	71.7	364	22	ABK68353	Drosophila melanog
41	33	71.7	523	22	ABG28286	Novel human diago
42	33	71.7	627	18	AAW17885	Photocorhabdus lum
43	33	71.7	627	18	AAW56544	Toxin Tcabi, encod
44	33	71.7	1189	18	AAW17884	Photocorhabdus lum
45	33	71.7	1189	19	AAW56543	Toxin Tcab, encode

ALIGNMENTS

RESULT 1	ABG60827	standard; Peptide; 10 AA.
XX	ABG60827	
AC	ABG60827	
XX		
DT	13-AUG-2002	(first entry)
XX		
XX		
DE	Hyaluronan (HA) binding peptide #10.	
XX		
KW	Tissue disorder; response-to-injury process; cell proliferating;	
KW	hyaluronin acid; HA; receptor for hyaluronan-mediated motility;	
KW	RHAMM; inflammatory neurological disorder; Parkinson's disease;	
KW	Alzheimer's disease; arthritis; multiple sclerosis; gastritis; nephritis;	
KW	inflammatory dermatosis; psoriasis; inflammatory bowel disease;	
KW	stenosis; restenosis; cancer; kidney fibrosis; inflammatory lung disease;	
KW	emphysema; asthma; cystic fibrosis; obesity; obesity related disease;	
KW	lupus; cardiovascular disease; atherosclerosis; wound; scar; diabetes;	
KW	tissue transplantation; stroke; inflammatory response; fibrotic response;	
KW	medical implant; Acquired immunodeficiency syndrome; AIDS; hepatitis;	
KW	myocardial fibrosis; hepatic fibrosis; chronic cystitis; acute mastitis;	
KW	septic shock; thyroiditis; retinopathy.	
XX		
OS	Synthetic.	
XX		
PN	WO200228415-A1.	
XX		
PD	11-APR-2002.	
XX		
PF	05-OCT-2000; 2000WO-IB01534.	
XX		
XX	05-OCT-2000; 2000WO-IB01534.	
XX		

PA (TRAN-) TRANSITION THERAPEUTICS & DIAGNOSTICS IN.
 XX
 XX
 PI Turley EA, Cruz TF;
 XX
 XX
 DR WPI: 2002-435298/46.
 XX
 PT Treating tissue disorder associated with response-to-injury process or
 PT proliferating cells in mammals, e.g. fibrosis, inflammation, by
 PT administering a compound that alters activity of transition molecules
 PT within a cell
 XX
 PS Example 31, Page 115, 215pp; English.
 XX
 XX The invention describes a method of treating a tissue disorder associated
 CC with response-to-injury process or proliferating cells in a patient,
 CC comprising administering a polypeptide (I) which binds hyalurononic acid
 CC (HA), an antibody which binds one of domains D1-D5 of Receptor for
 CC hyaluronon-mediated motility (RHAMM), a polypeptide fragment encoding
 CC any of D1-D5 of RHAMM, or a vector which expresses antisense RHAMM,
 CC antibodies or a polypeptide fragment. The method is useful for treating a
 CC patient with an inflammatory neurological disorder such as Parkinson's
 CC disease, Alzheimer's disease, arthritis including rheumatoid arthritis,
 CC osteoarthritis, multiple sclerosis, inflammatory dermatosis (psoriasis),
 CC inflammatory bowel disease, stenosis or restenosis, cancer, kidney
 CC fibrosis, inflammatory lung disease (e.g. emphysema, asthma, cystic
 CC fibrosis), obesity or obesity related diseases, lupus, cardiovascular
 CC disease (e.g. atherosclerosis), and wound especially surgical excision
 CC adhesions, to prevent scar and also for treating or preventing diabetes
 CC mellitus. The method is also useful for treating tissue transplantation
 CC (e.g. skin grafts), stroke, inflammatory responses or fibrotic response
 CC associated with medical implants such as hip implants, vascular wraps and
 CC catheters), inflammatory diseases such as AIDS, myocardial and hepatic
 CC fibrosis, chronic cystitis, acute mastitis, gastritis, nephritis,
 CC hepatitis, septic shock, thyroiditis, and retinopathy. This sequence
 CC represents a hyaluronon (HA) binding peptide used in the method of
 CC treating a tissue disorder described in the invention.
 CC
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 46; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 KXKSQLVKRX 10
 |||||
 Db 1 KXKSQLVKRX 10
 |||||
 RESULT 2
 AAR46551
 ID AAR46551 standard; Protein; 10 AA.
 XX
 AC AAR46551;
 XX
 DT 05-APR-1994 (first entry)
 XX
 DE Hyaluronan receptor binding motif (claimed).
 XX
 KW Hyaluronan binding protein; HA; RHAMM; mediated motility; wound;
 KW healing; diagnosis; treatment; cell locomotion; tumour invasion;
 KW birth defects; inflammatory disorder; Alzheimer's disease; dementia;
 KW Parkinson's disease; Huntington's disease; AIDS; diabetes; auto;
 KW immune diseases; corneal dysplasia; hypertrophy; surgery; burns;
 KW strokes; multiple sclerosis; depression; schizophrenia; CNS;
 KW contraception; in vitro fertilisation; embryo development.
 XX
 XX WO9321312-A.
 XX
 PD 28-OCT-1993.
 XX
 PF 13-APR-1993; 93WO-CA00158.
 XX
 PR 09-APR-1992; 92GB-0007949.

XX
 PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
 PA (UTMA-) UNIV MANITOBA.
 XX
 XX
 PI Turley EA;
 XX
 XX
 DR WPI: 1993-351722/44.
 XX
 PT DNA encoding hyaluronan receptor - used to produce proteins and
 PT antibodies for alteration of cell locomotion
 XX
 PS Claim 18; Page 57; 88pp; English.
 XX
 XX The sequence is that of a binding motif fragment of the hyaluronan
 CC receptor (HARC). HARC is down regulated in normal cells and is only
 CC expressed in situations where cell motility is desired, e.g. in
 CC wound healing, in response to growth factors and in chemotaxis by
 CC white blood cells. HA may be used for diagnosis and treatment of
 CC diseases involving cell locomotion, e.g. tumour invasion, birth
 CC defects, acute and chronic inflammatory disorders, Alzheimer's and
 CC other forms of dementia, AIDS, diabetes, autoimmune diseases, corneal
 CC dysplasias and hypertrophies, burns, surgical incisions and adhesions,
 CC strokes, multiple sclerosis, depression/schizophrenia related to
 CC neuronal growth and pain states involving nerve sprouting; also in CNS
 CC and spinal cord regeneration, contraception, in vitro fertilisation and
 CC embryo development.
 CC See also AAR46548-50 and AAR43563.
 CC
 XX
 SQ Sequence 10 AA;
 Query Match 93.5%; Score 43; DB 14; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.097;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 1 KXKSQLVKRX 10
 |||||
 Db 1 KXKSQLVKRX 10
 |||||
 RESULT 3
 AAM39164
 ID AAM39164 standard; peptide; 10 AA.
 XX
 AC AAM39164;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Mouse RHAMM binding domain 2 consensus motif peptide.
 XX
 KW Hyaluronan receptor; receptor for hyalurononic acid mediated motility;
 KW RHAMM; glycosaminoglycan; binding domain; mouse; oncogene; treatment;
 KW growth factor; cell locomotion disorder; dementia; detection;
 KW inflammatory disorder; autoimmune disease; diagnosis; prognosis.
 XX
 OS Mus sp.
 XX
 XX WO9738098-A1.
 XX
 PD 16-OCT-1997.
 XX
 PF 10-APR-1997; 97WO-CA00240.
 XX
 PR 10-APR-1996; 96GB-0007441.
 XX
 PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
 PA (UTMA-) UNIV MANITOBA.
 XX
 PI Entwistle J, Turley EA;
 XX
 XX WPI: 1997-512715/47.
 XX
 PT Isolated human receptor for hyalurononic acid mediated motility - used
 PT to develop products for treating e.g. tumours, inflammatory

PT disorders, dementia, AIDS, diabetes and auto-immune diseases
XX
PS Disclosure; Fig 1; 66pp; English.
XX
CC This peptide represents a motif found in a binding domain of mouse
CC hyaluronan receptor corresponding to amino acid position 424-433. This
CC receptor is also known as the receptor for hyaluronin acid mediated
CC motility (RHAMM). Hyaluronan is a large glycosaminoglycan that is
CC ubiquitous in the extracellular matrix and whose synthesis has been
CC linked to cell migration, growth and transformation. It interacts with
CC cell surfaces via specific protein receptors, e.g. RHAMM, that mediate
CC many biological effects. The RHAMM/hyaluronic acid interaction is
CC involved in oncogene and growth factor-mediated cell locomotion. The
CC products can be used in the treatment of disorders involving cell
CC locomotion, e.g. tumour invasion, birth defects, acute and chronic
CC inflammatory disorders, Alzheimer's and other forms of dementia,
CC including Parkinson's and Huntington's diseases, AIDS, diabetes,
CC autoimmune diseases, corneal dysplasia and hypertrophies, burns, surgical
CC incisions and adhesions, strokes and multiple sclerosis. They can also
CC be used in e.g. CNS and spinal cord regeneration, contraception and in
CC vitro fertilisation and embryo development. The products can also be
CC used in detection, diagnosis and prognosis.
XX
SQ Sequence 10 AA;
Query Match 93.5%; Score 43; DB 18; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.097;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLKSQLVVRK 10
||:|||||
Db 1 KLKSQLVVRK 10
RESULT 4
ABG60822
ID ABG60822 standard; Peptide; 11 AA.
XX
AC ABG60822;
XX
DT 13-AUG-2002 (first entry)
XX
DE Cellular response to injury associated peptide #3.
XX
KM Tissue disorder; response-to-injury process; cell proliferating;
KM hyaluronic acid; HA; receptor for hyaluronan-mediated motility;
KM RHAMM; inflammatory neurological disorder; Parkinson's disease;
KM Alzheimer's disease; arthritis; multiple sclerosis; gastritis; nephritis;
KM inflammatory dermatosis; psoriasis; inflammatory bowel disease;
KM stenosis; restenosis; cancer; kidney fibrosis; inflammatory lung disease;
KM emphysema; asthma; cystic fibrosis; obesity; obesity related disease;
KM lupus; cardiovascular disease; atherosclerosis; wound; scar; diabetes;
KM tissue transplantation; stroke; inflammatory response; fibrotic response;
KM medical implant; Acquired immunodeficiency syndrome; AIDS; hepatitis;
KM myocardial fibrosis; hepatic fibrosis; chronic cystitis; acute mastitis;
KM septic shock; thyroiditis; retinopathy.
XX
OS Homo sapiens.
XX
PN WO200228415-A1.
XX
PD 11-APR-2002.
XX
PF 05-OCT-2000; 2000WO-IB01534.
XX
PR 05-OCT-2000; 2000WO-IB01534.
XX
PA (TRAN-) TRANSITION THERAPEUTICS & DIAGNOSTICS IN.
XX
PI Turley BA, Cruz TF;
XX
XX WPI; 2002-435298/46.
XX

PT Treating tissue disorder associated with response-to-injury process or
PT proliferating cells in mammals, e.g. fibrosis, inflammation, by
PT administering a compound that alters activity of transition molecules
PT within a cell
XX
PS Disclosure; Page 199; 215pp; English.
XX
XX The invention describes a method of treating a tissue disorder associated
CC with response-to-injury process or proliferating cells in a patient,
CC comprising administering a polypeptide (I) which binds hyaluronic acid
CC (HA), an antibody which binds one of domains D1-D5 of Receptor for
CC hyaluronan-mediated motility (RHAMM), a polypeptide fragment encoding
CC any of D1-D5 of RHAMM, or a vector which expresses antisense RHAMM,
CC antibodies or a polypeptide fragment. The method is useful for treating a
CC patient with an inflammatory neurological disorder such as Parkinson's
CC disease, Alzheimer's disease, arthritis including rheumatoid arthritis,
CC osteoarthritis, multiple sclerosis, inflammatory dermatosis (psoriasis),
CC inflammatory bowel disease, stenosis or restenosis, cancer, kidney
CC fibrosis, inflammatory lung disease (e.g. emphysema, asthma, cystic
CC fibrosis), obesity or obesity related diseases, lupus, cardiovascular
CC disease (e.g. atherosclerosis), and wound especially surgical excision
CC adhesions, to prevent scar and also for treating or preventing diabetes
CC mellitus. The method is also useful for treating tissue transplantation
CC (e.g. skin grafts), stroke, inflammatory responses or fibrotic response
CC associated with medical implants such as hip implants, vascular wraps and
CC catheters), inflammatory diseases such as AIDS, myocardial and hepatic
CC fibrosis, chronic cystitis, acute mastitis, gastritis, nephritis,
CC hepatitis, septic shock, thyroiditis, and retinopathy. This sequence
CC represents a peptide associated with the method of treating tissue
disorders described in the invention.
XX
SQ Sequence 11 AA;
Query Match 93.5%; Score 43; DB 23; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.11;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLKSQLVVRK 10
||:|||||
Db 1 KLKSQLVVRK 10

RESULT 5
AAR9677
ID AAR9677 standard; Protein; 32 AA.
XX
AC AAR9677;
XX
DT 10-OCT-1996 (first entry)
XX
DE Hyaluronan binding domain of RHAMM.
XX
KM RHAMM 1; receptor for hyaluronic acid mediated motility;
KM hyaluronan receptor; cell locomotion; cell proliferation;
KM breast cancer; therapy; dominant suppressor mutant.
XX
OS Mus sp.
XX
FH Key Location/Qualifiers
FH Domain 1..11 /label= HA_binding_domain_1
FH /note= "corresponds to amino acids 532-542 of
FH RHAMM"
FT Domain 23..32 /label= HA_binding_domain_II
FT /note= "corresponds to amino acids 553-562 of
FT RHAMM"
PN EP721012-A2.
XX
PD 10-JUL-1996.
XX
PF 16-OCT-1995; 95EP-0307310.
XX

```
XX 14-OCT-1994; 94GB-0020740.
XX
XX (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
XX PA (UWMA-) UNIV MANITOBA.
XX
XX PI Entwistle J, Turley EA, Zhang S;
XX
XX WPI; 1996-310997/32.
XX DR N-PSDB; AAT34500;
XX DR N-PSDB; AAT34423;
XX DR N-PSDB; AAT34524.
XX
XX Receptor for hyaluronidic acid-mediated motility protein, and DNA
XX encoding it - useful to treat or prevent diseases associated with
XX the receptor, e.g. breast cancer
XX
XX PS Example 6; Fig 18A; 117pp; English.
XX
XX The hyaluronan (HA) binding domains (AAR99677) of receptor for
XX CC hyaluronidic acid-mediated motility protein, RHAMM 1 (AAR99673), were
XX CC mutated (see also AAR99678) in order to determine the importance of
XX CC RHAMM for maintenance of the transformed phenotype of H-ras-transformed
XX CC fibrosarcomas. Loss of HA binding was confirmed for the mutated
XX CC RHAMM fusion protein in a transfect assay. Reversion of
XX CC H-ras-transformation with the mutated RHAMM was demonstrated.
XX CC Dominant suppressor mutants of the RHAMM gene may be used in the
XX CC treatment or prevention of disorders characterised by RHAMM gene
XX CC overexpression, e.g. breast cancer.
XX
XX SQ Sequence 32 AA;
XX
XX Query Match 93.5%; Score 43; DB 17; Length 32;
XX Best Local Similarity 90.0%; Pred. No. 0.3;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KXKSQLVKRX 10
XX ||:|||||
XX DB 23 KLRSQLVKRX 32
XX
XX RESULT 6
XX ABG60846
XX ID ABG60846 standard; Peptide; 32 AA.
XX
XX AC ABG60846;
XX
XX DT 13-AUG-2002 (first entry)
XX
XX DE Receptor for hyalauronan-mediated motility binding peptide #2.
XX
XX KW Tissue disorder; response-to-injury process; cell proliferation;
XX KW hyaluronidic acid; HA; receptor for hyalauronan-mediated motility;
XX KW RHAMM; inflammatory neurological disorder; Parkinson's disease;
XX KW Alzheimer's disease; arthritis; multiple sclerosis; gastritis; nephritis;
XX KW inflammatory dermatosis; psoriasis; inflammatory bowel disease;
XX KW stenosis; restenosis; cancer; kidney fibrosis; inflammatory lung disease;
XX KW emphysema; asthma; cystic fibrosis; obesity; obesity related disease;
XX KW lupus; cardiovascular disease; atherosclerosis; wound; scar; diabetes;
XX KW tissue transplantation; stroke; inflammatory response; fibrotic response;
XX KW medical implant; Acquired immunodeficiency syndrome; AIDS; hepatitis;
XX KW myocardial fibrosis; hepatic fibrosis; chronic cystitis; acute mastitis;
XX KW septic shock; thyroiditis; retinopathy.
XX
XX OS Unidentified.
XX
XX WO200228415-A1.
XX
XX 11-APR-2002.
XX
XX PD 05-OCT-2000; 2000WO-IB01534.
XX
XX PF 05-OCT-2000; 2000WO-IB01534.
XX
XX PR
```

```
XX (TRAN-) TRANSITION THERAPEUTICS & DIAGNOSTICS IN.
XX PA Turley EA, Cruz TF;
XX PI WPI; 2002-435298/46.
XX
XX DR WPI; 2002-435298/46.
XX
XX KW Treating tissue disorder associated with response-to-injury process or
XX KW proliferating cells in mammals, e.g. fibrosis, inflammation, by
XX KW administering a compound that alters activity of transition molecules
XX KW within a cell -
XX
XX PS Example 11; Page 89; 215pp; English.
XX
XX The invention describes a method of treating a tissue disorder associated
XX CC with response-to-injury process or proliferating cells in a patient,
XX CC comprising administering a polypeptide (I) which binds hyaluronidic acid
XX CC (HA), an antibody which binds one of domains D1-D5 of Receptor for
XX CC hyalauronan-mediated motility (RHAMM), a polypeptide fragment encoding
XX CC any of D1-D5 of RHAMM, or a vector which expresses antisense RHAMM,
XX CC antibodies or a polypeptide fragment. The method is useful for treating a
XX CC patient with an inflammatory neurological disorder such as Parkinson's
XX CC disease, Alzheimer's disease, arthritis including rheumatoid arthritis,
XX CC osteoarthritis, multiple sclerosis, inflammatory dermatosis (psoriasis),
XX CC inflammatory bowel disease, stenosis or restenosis, cancer, kidney
XX CC fibrosis, inflammatory lung disease (e.g. emphysema, asthma, cystic
XX CC fibrosis), obesity or obesity related diseases, lupus, cardiovascular
XX CC disease (e.g. atherosclerosis), and wound especially surgical excision
XX CC adhesions, to prevent scar and also for treating or preventing diabetes
XX CC mellitus. The method is also useful for treating tissue transplantation
XX CC (e.g. skin grafts), stroke, inflammatory responses or fibrotic response
XX CC associated with medical implants such as hip implants, vascular wraps and
XX CC catheters), inflammatory diseases such as AIDS, myocardial wraps and
XX CC fibrosis, chronic cystitis, acute mastitis, gastritis, nephritis,
XX CC hepatitis, septic shock, thyroiditis, and retinopathy. This sequence
XX CC represents a receptor for hyalauronan-mediated motility binding peptide
XX CC used in the method of treating a tissue disorder described in the
XX CC invention.
XX
XX SQ Sequence 32 AA;
XX
XX Query Match 93.5%; Score 43; DB 23; Length 32;
XX Best Local Similarity 90.0%; Pred. No. 0.3;
XX Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 KXKSQLVKRX 10
XX ||:|||||
XX DB 23 KLRSQLVKRX 32
XX
XX RESULT 7
XX AAR43563
XX ID AAR43563 standard; Protein; 476 AA.
XX
XX AC AAR43563;
XX
XX DT 05-APR-1994 (first entry)
XX
XX DE Hyaluronan receptor.
XX
XX KW Hyaluronan binding protein; HA; RHAMM; mediated motility; wound;
XX KW healing; diagnosis; treatment; cell locomotion; tumour invasion;
XX KW birth defects; inflammatory disorder; Alzheimer's disease; dementia;
XX KW Parkinson's disease; Huntington's disease; AIDS; diabetes; auto;
XX KW immune diseases; corneal dysplasia; hypertrophy; surgery; burns;
XX KW strokes; multiple sclerosis; depression; schizophrenia; CND;
XX KW contraception; in vitro fertilisation; embryo development.
XX
XX WO9321312-A.
XX
XX 28-OCT-1993.
XX
XX PD 13-APR-1993; 93WO-CA00158.
XX
XX PF
```

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XX 09-APR-1992; 92GB-0007949.
PR (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
PA (YVMA-) UNIV MANITOBA.
PI Turley EA;
XX WPI; 1993-351722/44.
DR N-PSDB; AA051212.
XX
XX DNA encoding hyaluronan receptor - used to produce proteins and
PT antibodies for alteration of cell locomotion
XX
XX Claim 7; Fig 23; 88bp; English.
XX
XX The sequence is that encoded by a cDNA clone encoding the hyaluronan
CC receptor (HARC). The sequence was obtd. by screening a 373 library in
CC lambda gill with antibodies to HARC. A clone of 1.9 kb was obtained
CC and used to rescreen the library to obtain the full length, 2.9 kb
CC clone. HA is down regulated in stationary normal cells and is only
CC expressed in situations where cell motility is desired, e.g. in
CC wound healing, in response to growth factors and in chemotaxis by
CC white blood cells. HA may be used for diagnosis and treatment of
CC diseases involving cell locomotion, e.g. tumour invasion, birth
CC defects, acute and chronic inflammatory disorders, Alzheimer's and
CC other forms of dementia, AIDS, diabetes, autoimmune diseases, corneal
CC dysplasias and hypertrophies, burns, surgical incisions and adhesions,
CC strokes, multiple sclerosis, depression/schizophrenia related to
CC neuronal growth and pain states involving nerve sprouting; also in CNS
CC and spinal cord regeneration, contraception, in vitro fertilisation and
CC embryo development.
CC See also AAR46548-51.
XX
XX Sequence 476 AA;
SQ
Query Match 93.5%; Score 43; DB 14; Length 476;
Best Local Similarity 90.0%; Pred. No. 4.2;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLRSQLVYRK 10
Db 423 KLRSQLVYRK 432

```

RESULT 8
AAR9673
ID AAR9673 standard; Protein; 606 AA.

```

XX AAR9673;
AC 10-OCT-1996 (first entry)
XX
XX Receptor for hyaluronic acid mediated motility RHAMM 1.
DE
XX RHAMM 1; receptor for hyaluronic acid mediated motility;
KM hyaluronan receptor; cell locomotion; cell proliferation;
XX breast cancer; therapy.
XX
XX Mus BP.
OS
XX
XX Key Location/Qualifiers.
FH 91..93
FT Modified-site /label= N-glycosylation_site
FT 258..260
FT Modified-site /label= N-glycosylation_site
FT 279..281
FT Modified-site /label= N-glycosylation_site
FT 300..302
FT Modified-site /label= N-glycosylation_site
FT 321..323
FT Modified-site /label= N-glycosylation_site
FT 342..344
FT Modified-site

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FT Modified-site /label= N-glycosylation_site
FT 373..375
FT Modified-site /label= N-glycosylation_site
FT 413..415
FT Modified-site /label= N-glycosylation_site
FT 532..542
FT Domain /label= Hyaluronan_binding_domain-1
FT 553..562
FT Domain /label= Hyaluronan_binding_domain-1
FT 594..596
FT Modified-site /label= Hyaluronan_binding_domain-1
FT 594..596
FT /label= N-glycosylation_site
XX
XX EP721012-A2.
XX
XX 10-JUL-1996.
XX
XX 16-OCT-1995; 95EP-0307310.
XX
XX 14-OCT-1994; 94GB-0020740.
XX
XX (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
PA (YVMA-) UNIV MANITOBA.
XX
XX Entwistle J, Turley EA, Zhang S;
PI
XX WPI; 1996-310997/32.
XX
XX N-PSDB; AAT34499;
DR N-PSDB; AAT34500;
DR N-PSDB; AAT34523;
DR N-PSDB; AAT34524.
XX
XX Receptor for hyaluronic acid-mediated motility protein, and DNA
PT encoding it - useful to treat or prevent diseases associated with
PT the receptor, e.g. breast cancer
XX
XX Claim 2; Page 40-42; 117bp; English.
XX
XX RHAMM 1 (AAR9673), or Receptor for Hyaluronic Acid Mediated Motility,
CC is a hyaluronan receptor protein which is involved in cell locomotion
CC or motility and cell proliferation and transformation. Its amino
CC acid sequence was deduced from a cDNA clone (AAT34499) obtd. from
CC murine 3T3 cells and a genomic sequence (AAT34500) from a mouse
CC fibroblast genomic library. 2 Alternative mRNAs for RHAMM 1 were
CC found, RHAMM 1A (see also AAT34523) and RHAMM 1B (AAT34524), that had
CC identical translated portions. Increased expression of RHAMM 1
CC protein is indicative of a poor prognosis for breast cancer. The
CC protein can be used to suppress or control a tumour by modulating
CC the interaction of cell-associated RHAMM with its ligand.
XX
XX Sequence 606 AA;
SQ
Query Match 93.5%; Score 43; DB 17; Length 606;
Best Local Similarity 90.0%; Pred. No. 5.3;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLRSQLVYRK 10
Db 553 KLRSQLVYRK 562

```

RESULT 9
AAM39166
ID AAM39166 standard; Protein; 630 AA.

```

XX AAM39166;
AC 27-APR-1998 (first entry)
XX
XX Mouse RHAMM protein.
DE
XX Hyaluronan receptor; receptor for hyaluronic acid mediated motility;
KM RHAMM; glycosaminoglycan; binding domain; mouse; oncogene; treatment;
XX growth factor; cell locomotion disorder; dementia; detection;

```

Key	Location/Qualifiers
OS	Mus sp.
XX	
XX	
FH	Region
FT	279..382
FT	/note="repeat region"
FT	555..565
FT	/note="Hyaluronic acid binding domain"
FT	577..586
FT	/note="Hyaluronic acid binding domain"
XX	
XX	
PN	WO9738098-A1.
XX	
PD	16-OCT-1997.
XX	
XX	
PF	10-APR-1997;
XX	97WO-CA00240.
XX	
PR	10-APR-1996;
XX	96GB-0007441.
XX	
PA	(MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
XX	(UYMA-) UNIT MANITOBA.
XX	
PI	Entwistle J, Turley EA;
XX	
DR	WPI; 1997-512715/47.
DR	N-PSDB; AAV02801.
XX	
PT	Isolated human receptor for hyaluronic acid mediated motility - used
PT	to develop products for treating e.g. tumours, inflammatory
PT	disorders, dementia, AIDS, diabetes and auto-immune diseases
XX	
XX	
PS	Disclosure; Page 46; 66pp; English.
XX	
XX	
CC	This sequence represents the mouse hyaluronan receptor which is also
CC	known as the receptor for hyalurononic acid mediated motility (RHAMM).
CC	Hyaluronan is a large glycosaminoglycan that is ubiquitous in the
CC	extracellular matrix and whose synthesis has been linked to cell
CC	migration, growth and transformation. It interacts with cell surfaces via
CC	specific protein receptors, e.g. RHAMM, that mediate many biological
CC	effects. The RHAMM/Hyaluronic acid interaction is involved in
CC	oncogene- and growth factor-mediated cell locomotion. The products can be
CC	used in the treatment of disorders involving cell locomotion, e.g. tumour
CC	invasion, birth defects, acute and chronic inflammatory disorders,
CC	Alzheimer's and other forms of dementia, including Parkinson's and
CC	Huntington's diseases, AIDS, diabetes, autoimmune diseases, corneal
CC	dysplasia and hypertrophies, burns, surgical incisions and adhesions,
CC	strokes and multiple sclerosis. They can also be used in e.g. CNS and
CC	spinal cord regeneration, contraception and in vitro fertilisation and
CC	embryo development. The products can also be used in detection, diagnosis
CC	and prognosis.
XX	
XX	
SO	Sequence 630 AA;
QY	
DB	577 KLRSQLVKKR 586
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY	1 KLRSQLVKKR 10
DB	577 KLRSQLVKKR 586
QY	93.5%; Score 43; DB 18; Length 630;
DB	Best Local Similarity 90.0%; Pred. No. 5.5;
QY	Matches 9; Conservative 1; Mismatches 0; Indels 0; G

KW	RHAMM 1-2a; receptor for hyaluronic acid mediated motility;
KW	hyaluronan receptor; cell locomotion; cell proliferation;
KW	breast cancer; therapy.
XX	
OS	Mus sp.
XX	
FH	Key Location/Qualifiers
FT	Region 55..79
FT	/note= "exon 2A-encoded region"
XX	
PX	EP721012-A2.
PN	10-JUL-1996.
PD	
PF	16-OCT-1995; 95EP-0307310.
PP	
PR	14-OCT-1994; 94GB-0020740.
PS	
PA	(MANI-) MANITOBA CANCER TREATMENT & RES FOUND. (UTMA-) UNIV MANITABA.
PI	Entwistle J, Turley EA, Zhang S; MPI:1996-310997/32. N-P8DB; AAT34525.
DR	
NB	Receptor for hyaluronic acid-mediated motility protein, and DNA encoding it - useful to treat or prevent diseases associated with the receptor, e.g. breast cancer
PT	
PR	Claim 8; Page 50-52; 11pp; English.
PS	
CX	RHAMM 1-2a (AA99675) is an alternatively spliced variant of RHAMM 1 (AA99673) (receptor for hyaluronic acid mediated motility), a protein involved in cell locomotion or motility and cell proliferation and transformation. It differs from RHAMM 1 by an insertion of 25 amino acids (see also AA99674) between amino acids 54 and 55 of RHAMM 1, resulting from an alternative splicing exon 2A (AA734502). RHAMM 1-2a is the isoform that is overexpressed in tumours. Determination of the level of RHAMM 1-2a in a sample can be used to assess the prognosis of a tumour (esp. breast cancer) patient. The RHAMM 1-2a protein can also be used to suppress or control a tumour by modulating the interaction of cell-associated RHAMM with its ligand.
CC	
CC	
CC	
SQ	Sequence 631 AA;
Query Match	93.5%; Score 43; DB 17; Length 631;
Best Local Similarity	90.0%; Pred. No. 5.5;
Matches 9; Conservative	1; Mismatches 0; Indels 0; Gaps 0.
OY	1 KLRKSLVKRK 10 : Db 578 KLRKSLVKRK 587
RESULT 11	
AAG60843	ID AAG60843 standard; Protein: 631 AA.
AC	AAG60843;
DT	13-AUG-2002 (first entry)
DE	Mouse receptor for hyalauronan-mediated motility (RHAMM).
Tissue disorder; response-to-injury process; cell proliferating;	
hyaluronic acid; HA; receptor for hyaluronan-mediated motility;	
RHAMM; inflammatory neurological disorder; Parkinson's disease;	
Alzheimer's disease; arthritis; multiple sclerosis; gastritis; nephritis;	
Inflammatory dermatosis; psoriasis; Inflammatory bowel disease;	
stenosis; restenosis; cancer; kidney fibrosis; inflammatory lung disease;	
emphysema; asthma; cystic fibrosis; obesity; obesity related disease;	

KW lupus; cardiovascular disease; atherosclerosis; wound; scar; diabetes;
 KW tissue transplantation; stroke; inflammatory response; fibrotic response;
 KW medical implant; Acquired immunodeficiency syndrome; AIDS; hepatitis;
 KW myocardial fibrosis; hepatic fibrosis; chronic cystitis; acute mastitis;
 KW septic shock; thyroiditis; retinopathy.
 XX
 OS Mus musculus.
 XX
 XX WO200228415-A1.
 XX
 XX 11-Apr-2002.
 XX
 XX 05-Oct-2000; 2000WO-IB01534.
 XX
 XX 05-Oct-2000; 2000WO-IB01534.
 XX
 XX (TRAN-) TRANSITION THERAPEUTICS & DIAGNOSTICS IN.
 XX
 XX Turley EA, Cruz TF;
 XX
 XX WPI; 2002-435298/46.
 XX
 XX
 PT Treating tissue disorder associated with response-to-injury process or
 PT proliferating cells in mammals, e.g. fibrosis, inflammation, by
 PT administering a compound that alters activity of transistion molecules
 PT within a cell
 XX
 PS Disclosure; Fig 50; 215pp; English.
 XX
 CC The invention describes a method of treating a tissue disorder associated
 CC with response-to-injury process or proliferating cells in a patient,
 CC comprising administering a polypeptide (I) which binds hyaluronic acid
 CC (HA), an antibody which binds one of domains D1-D5 of Receptor for
 CC hyaluronan-mediated motility (RHAMM), a polypeptide fragment encoding
 CC any of D1-D5 of RHAMM, or a vector which expresses antisense RHAMM,
 CC antibodies or a polypeptide fragment. The method is useful for treating a
 CC patient with an inflammatory neurological disorder such as Parkinson's
 CC disease, Alzheimer's disease, arthritis including rheumatoid arthritis,
 CC osteoarthritis, multiple sclerosis, inflammatory dermatosis (psoriasis),
 CC inflammatory bowel disease, stenosis or restenosis, cancer, kidney
 CC fibrosis, inflammatory lung disease (e.g. emphysema, asthma, cystic
 CC fibrosis), obesity or obesity related diseases, lupus, cardiovascular
 CC disease (e.g. atherosclerosis), and wound especially surgical excision
 CC adhesions, to prevent scar and also for treating or preventing diabetes
 CC mellitus. The method is also useful for treating tissue transplantation
 CC (e.g. skin grafts), stroke, inflammatory responses or fibrotic response
 CC associated with medical implants such as hip implants, vascular wraps and
 CC catheters), inflammatory diseases such as AIDS, myocardial and hepatic
 CC fibrosis, chronic cystitis, acute mastitis, gastritis, nephritis,
 CC hepatitis, septic shock, thyroiditis, and retinopathy. This sequence
 CC represents a receptor for hyaluronan-mediated motility protein used in
 CC the method of treating a tissue disorder described in the invention.
 XX
 SQ Sequence 631 AA;
 Query Match 93.5%; Score 43; DB 23; Length 631;
 Best Local Similarity 90.0%; Pred. No. 5.5;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLSQGVYRK 10
 Db 578 KLSQGVYRK 587
 RESULT 12
 AAU11437
 ID AAU11437 standard; Proteins; 794 AA.
 XX
 AC AAU11437;
 XX
 XX 12-MAR-2002 (first entry)
 DT
 XX Mouse hyaluronic acid binding protein RHAMM.

XX
 KW Mouse; hyaluronic acid binding protein; RHAMM; gene therapy;
 KW receptor for HA mediated motility; immunosuppressive; cytostatic.
 KW conjugate; rheumatoid arthritis; scleroderma; liver fibrosis; cancer;
 XX
 OS Mus musculus.
 XX
 XX
 PH Key Location/Qualifiers
 XX
 FT MISC-difference 55 /note= "Encoded by AAC"
 FT MISC-difference 71 /note= "Encoded by ACG"
 FT MISC-difference 89. /note= "Encoded by CAA"
 FT MISC-difference 91 /note= "Encoded by CAC"
 FT MISC-difference 540 /note= "Encoded by ACT"
 FT MISC-difference 668 /note= "Encoded by GAT"
 FT
 XX
 XX WO200180899-A2.
 XX
 XX 01-NOV-2001.
 XX
 XX 20-APR-2001; 2001WO-CA00533.
 XX
 XX 20-APR-2000; 2000US-198613P.
 XX
 XX (CANG-) CANGENE CORP.
 XX
 XX Woloiski BMR, Williams AM, Sereda TJ, Wiebe DJ;
 XX
 XX WPI; 2002-075094/10.
 DR N-PSDB; AAS17497.
 PT
 PT Protein conjugates that selectively target certain tissues and organs
 PT useful for treating and preventing various diseases, comprises
 PT glucose-aminoglycan-targeting domain conjugated to a therapeutic
 PT protein
 XX
 XX Claim 6, Page 116; 121pp; English.
 PS
 XX
 CC The invention relates to a conjugate comprising an hyaluronic acid (HA)
 CC -binding protein e.g. RHAMM (receptor of HA mediated motility) or peptide
 CC contiguous with, or coupled to a polypeptide conjugated to a therapeutic
 CC agent, and the polynucleotides encoding them. Also included is a method
 CC for preparation of the HA-binding protein by inserting a first nucleotide
 CC sequence encoding a HA-binding protein directly linked to a second
 CC nucleotide sequence encoding a therapeutic protein into a suitable
 CC vector, expressing the vector in an acceptable host, purifying conjugate
 CC molecule from host or expression medium. The composition is useful for
 CC altering in vivo the distribution of a therapeutic agent comprising
 CC administering the composition to the animal where conjugate molecule will
 CC distribute primarily in tissues and organs containing high levels of
 CC endogenous HA and for treating mammal with a disorder where a diseased
 CC tissue of the mammal contains high level of HA e.g. rheumatoid
 CC arthritis, scleroderma, liver fibrosis and cancer. Lower therapeutic
 CC dosages regulated also translates into lower immunogenicity of the
 CC conjugated protein as compared to the native protein. As a result,
 CC conjugates improve patient compliance and reduce direct and indirect
 CC costs associated with the drug substance and its administration.
 CC Conjugates allows for the use, where appropriate, of lower, safer,
 CC dosages as compared to the conventional dosage requirements for the
 CC unconjugated corresponding therapeutic agent. Conjugate molecules have an
 CC increased half-life and potency, resulting in prolonged circulation of
 CC the molecule, efficient distribution into the target tissues, and
 CC increased bioavailability. The present sequence represents a RHAMM
 CC protein.
 XX
 SQ Sequence 794 AA;
 Query Match 93.5%; Score 43; DB 23; Length 794;

Best Local Similarity 90.0%; Pred. No. 6.8;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXKSQLVKKR 10
||:|||||
DB 741 KXRSQVKKR 750

RESULT 13
AAM39168
ID AAM39168 standard; peptide; 10 AA.

AC AAM39168;

DT 27-APR-1998 (first entry)

DE Rat RHAMM binding domain 2 consensus motif peptide.

KM Hyaluronan receptor; receptor for hyaluronic acid mediated motility;
KM RHAMM; glycosaminoglycan; binding domain; rat; oncogene; treatment;
KM growth factor; cell locomotion disorder; dementia; detection;
KM inflammatory disorder; autoimmune disease; diagnosis; prognosis.

OS Rat sp.

FN WO9738098-A1.

PD 16-OCT-1997.

PF 10-APR-1997; 97WO-CA00240.

PR 10-APR-1996; 96GB-0007441.

PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.

PA (UYMA-) UNIV MANITOBA.

PI Entwistle J, Turley EA;

DR WPI; 1997-512715/47.

PT Isolated human receptor for hyaluronic acid mediated motility - used
PT to develop products for treating e.g. tumours, inflammatory
PT disorders, dementia, AIDS, diabetes and auto-immune diseases
XX
XX
XX Disclosure; Fig 1; 66pp; English.

CC This peptide represents a motif found in a binding domain of rat
CC hyaluronan receptor corresponding to amino acid position 424-433. This
CC receptor is also known as the receptor for hyaluronic acid mediated
CC motility (RHAMM). Hyaluronan is a large glycosaminoglycan that is
CC ubiquitous in the extracellular matrix and whose synthesis has been
CC linked to cell migration, growth and transformation. It interacts with
CC cell surfaces via specific protein receptors, e.g. RHAMM, that mediate
CC many biological effects. The RHAMM/hyaluronic acid interaction is
CC involved in oncogene and growth factor-mediated cell locomotion. The
CC products can be used in the treatment of disorders involving cell
CC locomotion, e.g. tumour invasion, birth defects, acute and chronic
CC inflammatory disorders, Alzheimer's and other forms of dementia,
CC including Parkinson's and Huntington's diseases, AIDS, diabetes,
CC autoimmune diseases, corneal dysplasia and hypertropies, burns, surgical
CC incisions and adhesions, strokes and multiple sclerosis. They can also
CC be used in e.g. CNS and spinal cord regeneration, contraception and in
CC *in vitro* fertilisation and embryo development. The products can also be
CC used in detection, diagnosis and prognosis.

CC
XX
SQ Sequence 10 AA;

Query Match 84.8%; Score 39; DB 18; Length 10;
Best Local Similarity 80.0%; Pred. No. 0.55;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KXKSQLVKKR 10
||:|||||

DB 1 KXRSQVKKR 10

RESULT 14
AAU11438
ID AAU11438 standard; Protein; 713 AA.

AC AAU11438;

DT 12-MAR-2002 (first entry)

DE Rat hyaluronic acid binding protein RHAMM.

KM Rat; hyaluronic acid binding protein; RHAMM; gene therapy;
KM receptor for HA mediated motility; immunosuppressive; cytostatic.
KM conjugate; rheumatoid arthritis; scleroderma; liver fibrosis; cancer;

OS Rattus norvegicus.

FN WO200180899-A2.

PD 01-NOV-2001.

PF 20-APR-2001; 2001WO-CA00533.

PR 20-APR-2000; 2000US-198613P.

PA (CANG-) CANGENE CORP.

PI Woloski BMR, Williams AM, Sereda TJ, Wiebe DJ;

DR WPI; 2002-075094/10.

DR N-PSDB; AAS17498.

PT Protein conjugates that selectively target certain tissues and organs
PT useful for treating and preventing various diseases, comprises
PT glucose-aminoglycan-targeting domain conjugated to a therapeutic
PT protein -

XX
XX
XX Claim 6; Page 116-117; 121pp; English.

CC The invention relates to a conjugate comprising an hyaluronic acid (HA)
CC -binding protein e.g. RHAMM (receptor of HA mediated motility) or peptide
CC contiguous with, or coupled to a polypeptide conjugated to a therapeutic
CC agent, and the polynucleotides encoding them. Also included is a method
CC for preparation of the HA-binding protein by inserting a first nucleotide
CC sequence encoding a HA-binding protein directly linked to a second
CC nucleotide sequence encoding a therapeutic protein into a suitable
CC vector, expressing the vector in an acceptable host, purifying conjugate
CC molecule from host or expression medium. The composition is useful for
CC altering *in vivo* the distribution of a therapeutic agent comprising
CC administering the composition to the animal where conjugate molecule will
CC distribute primarily in tissues and organs containing high levels of
CC endogenous HA and for treating mammal with a disorder where a diseased
CC tissue of the mammal contains high level of HA e.g. rheumatoid
CC arthritis, scleroderma, liver fibrosis and cancer. Lower therapeutic
CC dosages required also translates into lower immunogenicity of the
CC conjugated protein as compared to the native protein. As a result,
CC conjugates improve patient compliance and reduce direct and indirect
CC costs associated with the drug substance and its administration.
CC Conjugates allows for the use, where appropriate, of lower, safer,
CC dosages as compared to the conventional dosage requirements for the
CC unconjugated corresponding therapeutic agent. Conjugate molecules have an
CC increased half-life and potency, resulting in prolonged circulation of
CC the molecule, efficient distribution into the target tissues, and
CC increased bioavailability. The present sequence represents a RHAMM
CC protein.

CC
XX
SQ Sequence 713 AA;

Query Match 84.8%; Score 39; DB 23; Length 713;
Best Local Similarity 80.0%; Pred. No. 35;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLRSQLVKK 10
|:|:|:|
Db 657 KLRSQLAKRK 666

RESULT 15

AAK46550
ID AAK46550 standard; Protein; 9 AA.

AC AAK46550;

DT 05-APR-1994 (first entry)

DE Hyaluronan receptor binding motif (claimed).

KW Hyaluronan binding protein; HA; RHAMM; mediated motility; wound;
KW healing; diagnosis; treatment; cell locomotion; tumour invasion;
KW birth defects; inflammatory disorder; Alzheimer's disease; dementia;
KW Parkinson's disease; Huntington's disease; AIDS; diabetes; auto;
KW immune diseases; corneal dysplasia; hypertrophy; surgery; burns;
KW strokes; multiple sclerosis; depression; schizophrenia; CNF;
KW contraception; in vitro fertilisation; embryo development.

PN W09321312-A.

PD 28-OCT-1993.

PF 13-APR-1993; 93WC-CA00158.

PR 09-APR-1992; 92GB-0007949.

PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
(UYMA-) UNIV MANITOBA.

PI Turley EA;

DR WPI; 1993-351722/44.

PT DNA encoding hyaluronan receptor - used to produce proteins and
antibodies for alteration of cell locomotion

PS Claim 17; Page 57; 88pp; English.

CC The sequence is that of a binding motif fragment of the hyaluronan
CC receptor (HARC). HARC is down regulated in normal cells and is only
CC expressed in situations where cell motility is desired, e.g. in
CC wound healing, in response to growth factors and in chemotaxis by
CC white blood cells. HA may be used for diagnosis and treatment of
CC diseases involving cell locomotion, e.g. tumour invasion, birth
CC defects, acute and chronic inflammatory disorders, Alzheimer's and
CC other forms of dementia, AIDS, diabetes, autoimmune diseases, corneal
CC dysplasias and hypertrophies, burns, surgical incisions and adhesions,
CC strokes, multiple sclerosis, depression/schizophrenia related to
CC neuronal growth and pain states involving nerve sprouting; also in CNJ
CC and spinal cord regeneration, contraception, in vitro fertilisation and
CC embryo development.
CC See also AAK46548-51 and AAK43563.

SC Sequence 9 AA;

Query Match 82.6%; Score 38; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLRSQLVKK 9
|:|:|:|
Db 1 KLRSQLVKK 9

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OM protein - protein search, using SW model

Run on: February 8, 2003, 10:42:50 ; Search time 7 Seconds
(without alignments)
31.670 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KIXSQLVKKR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/2/pubppaa/PCRUS_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	34	73.9	188	9	US-10-012-896-592
2	34	73.9	188	9	US-09-895-793-592
3	34	73.9	188	9	US-09-895-793-592
4	34	73.9	188	10	US-09-895-793-592
5	34	73.9	188	10	US-09-895-793-592
6	34	73.9	188	10	US-09-895-793-592
7	34	73.9	188	10	US-09-895-793-592
8	34	73.9	188	10	US-09-895-793-592
9	34	73.9	188	10	US-09-895-793-592
10	34	73.9	188	10	US-09-895-793-592
11	34	73.9	188	10	US-09-895-793-592
12	34	73.9	188	10	US-09-895-793-592
13	34	73.9	188	10	US-09-895-793-592
14	34	73.9	188	10	US-09-895-793-592
15	34	73.9	188	10	US-09-895-793-592
16	34	73.9	188	10	US-09-895-793-592
17	34	73.9	188	10	US-09-895-793-592
18	34	73.9	188	10	US-09-895-793-592
19	34	73.9	188	10	US-09-895-793-592
20	34	73.9	188	10	US-09-895-793-592

20	30	65.2	1224	10	US-09-801-368-222	Sequence 222, App
21	30	65.2	3169	9	US-10-114-170-257	Sequence 257, App
22	29	63.0	229	9	US-09-764-898-253	Sequence 253, App
23	29	63.0	421	10	US-09-841-133-577	Sequence 577, App
24	29	63.0	460	10	US-09-782-980-82	Sequence 82, App
25	29	63.0	460	10	US-09-884-430-6	Sequence 6, App
26	29	63.0	478	9	US-10-029-009-10	Sequence 10, App
27	29	63.0	488	9	US-10-029-009-22	Sequence 22, App
28	29	63.0	603	10	US-09-864-761-36676	Sequence 36676, A
29	29	63.0	621	10	US-09-856-247A-2	Sequence 2, App
30	29	63.0	835	10	US-09-801-574-22	Sequence 22, App
31	29	63.0	901	10	US-09-813-242-1148	Sequence 1148, A
32	29	63.0	909	10	US-09-925-299-988	Sequence 988, App
33	29	63.0	1185	9	US-09-895-913A-246	Sequence 246, App
34	29	63.0	2150	10	US-09-321-987B-2	Sequence 2, App
35	29	63.0	2165	10	US-09-800-729-155	Sequence 155, App
36	28	60.9	61	10	US-09-864-761-34874	Sequence 34874, A
37	28	60.9	64	10	US-09-815-242-11296	Sequence 11296, A
38	28	60.9	64	10	US-09-815-242-11475	Sequence 11475, A
39	28	60.9	127	9	US-09-764-868-801	Sequence 801, App
40	28	60.9	142	9	US-09-854-133-212	Sequence 212, App
41	28	60.9	142	10	US-09-738-973-212	Sequence 212, App
42	28	60.9	153	10	US-09-864-761-47313	Sequence 47313, A
43	28	60.9	160	10	US-09-764-864-1129	Sequence 1129, App
44	28	60.9	239	10	US-09-764-898-165	Sequence 165, App
45	28	60.9	273	9	US-09-738-626-5061	Sequence 5061, App

ALIGNMENTS

RESULT 1

US-10-012-896-592

Sequence 592, Application US/10012896

Publication No. US20020183251A1

GENERAL INFORMATION:

APPLICANT: Xu, Jiangchun

APPLICANT: Dillon, Jennifer L.

APPLICANT: Mitcham, Jennifer L.

APPLICANT: Harlocker, Susan L.

APPLICANT: Jiang, Yugu

APPLICANT: Katos, Michael D.

APPLICANT: Retter, Marc W.

APPLICANT: Stolk, John A.

APPLICANT: Day, Craig H.

APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick

APPLICANT: Li, Samuel X.

APPLICANT: Wang, Aijun

APPLICANT: Skeiky, Yasir A.W.

APPLICANT: Hepler, William T.

APPLICANT: Henderson, Robert A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Houghton, Raymond L.

APPLICANT: Vinals de Bassols, Carlota

APPLICANT: Foy, Teresa

APPLICANT: Fanger, Gary R.

APPLICANT: Wantanabe, Yoshihiro

APPLICANT: Meagher, Madeline Joy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

FILE REFERENCE: 210121.427C27

CURRENT APPLICATION NUMBER: US/10/012.896

CURRENT FILING DATE: 2001-12-10

NUMBER OF SEQ ID NOS: 1011

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 592

LENGTH: 188

TYPE: PRT

ORGANISM: Homo sapiens

US-10-012-896-592

Query Match 73.9%; Score 34; DB 9; Length 188;
 Best Local Similarity 77.8%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKSQVYRK 10
 Db 178 LKAQLVKOK 186

RESULT 2

US-09-895-793-592
 ; Sequence 592, Application US/09895793
 ; Publication No. US20020192763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stoik, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Baesols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.534C2
 ; CURRENT APPLICATION NUMBER: US/09/895,793
 ; CURRENT FILING DATE: 2001-06-29
 ; NUMBER OF SEQ ID NOS: 982
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 592
 ; LENGTH: 188
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-895-793-592

Query Match 73.9%; Score 34; DB 9; Length 188;
 Best Local Similarity 77.8%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKSQVYRK 10
 Db 178 LKAQLVKOK 186

RESULT 3

US-09-895-814-592
 ; Sequence 592, Application US/09895814
 ; Publication No. US20020193296A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stoik, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.

APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel X.
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William T.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Hural, John
 ; APPLICANT: McNeill, Patricia D.
 ; APPLICANT: Houghton, Raymond L.
 ; APPLICANT: Vinals de Baesols, Carlota
 ; APPLICANT: Foy, Teresa
 ; APPLICANT: Fanger, Gary R.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C26
 ; CURRENT APPLICATION NUMBER: US/09/895,814
 ; CURRENT FILING DATE: 2001-06-29
 ; NUMBER OF SEQ ID NOS: 990
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 592
 ; LENGTH: 188
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-895-814-592

Query Match 73.9%; Score 34; DB 9; Length 188;
 Best Local Similarity 77.8%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKSQVYRK 10
 Db 178 LKAQLVKOK 186

RESULT 4

US-09-759-143-592
 ; Sequence 592, Application US/09759143
 ; Patent No. US20020022248A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Xu, Jiangchun
 ; APPLICANT: Dillon, Davin C.
 ; APPLICANT: Mitcham, Jennifer L.
 ; APPLICANT: Harlocker, Susan L.
 ; APPLICANT: Jiang, Yuqiu
 ; APPLICANT: Kalos, Michael D.
 ; APPLICANT: Henderson, Robert A.
 ; APPLICANT: Fanger, Gary R.
 ; APPLICANT: Retter, Marc W.
 ; APPLICANT: Stoik, John A.
 ; APPLICANT: Day, Craig H.
 ; APPLICANT: Vedvick, Thomas S.
 ; APPLICANT: Carter, Darrick
 ; APPLICANT: Li, Samuel
 ; APPLICANT: Wang, Aijun
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Hepler, William
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
 ; TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
 ; FILE REFERENCE: 210121.427C23
 ; CURRENT APPLICATION NUMBER: US/09/759,143
 ; CURRENT FILING DATE: 2001-01-12
 ; NUMBER OF SEQ ID NOS: 934
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 592
 ; LENGTH: 188
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-09-759-143-592

Query Match 73.9%; Score 34; DB 10; Length 188;
 Best Local Similarity 77.8%; Pred. No. 16;
 Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKSQLVYRK 10
Db 178 LKSQLVYRK 186

RESULT 5

US-09-780-669-592
; Sequence 592, Application US/09780669
; Patent No. US20020051977A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yugu
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kaloe, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Rietter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darriek
; APPLICANT: Li, Samuel
; APPLICANT: Wang, Aljun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Hepler, William
; APPLICANT: Hurst, John
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Houghton, Raymond L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C24
; CURRENT APPLICATION NUMBER: US/09/780,669
; CURRENT FILING DATE: 2001-02-09
; NUMBER OF SEQ ID NOS: 943
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 592
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-780-669-592

Query Match 73.9%; Score 34; DB 10; Length 188;
Best Local Similarity 77.8%; Pred. No. 16;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKSQLVYRK 10
Db 178 LKSQLVYRK 186

RESULT 6

US-09-822-827-592
; Sequence 592, Application US/09822827
; Patent No. US20020081680A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.534C1
; CURRENT APPLICATION NUMBER: US/09/822,827
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 982
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 592
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-822-827-592

Query Match 73.9%; Score 34; DB 10; Length 188;
Best Local Similarity 77.8%; Pred. No. 16;

Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
Qy 2 LKSQLVYRK 10
Db 178 LKSQLVYRK 186

RESULT 7
US-09-864-761-46169
; Sequence 46169, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 4917
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 46169
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC009275.5
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
; OTHER INFORMATION: EXPRESSED IN SWISSPROT HIT: P15121, EVALUATE 4.00e-26
; OTHER INFORMATION: EST_HUMAN HIT: BE257210.1, EVALUATE 5.00e-25
US-09-864-761-46169

Query Match 69.6%; Score 32; DB 10; Length 55;
Best Local Similarity 60.0%; Pred. No. 10;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Cy 1 KXKSQLVYRK 10
Db 39 KLRQGVYRK 48

RESULT 8
US-09-864-761-33351
Sequence 33351, Application US/09864761
Patent No. US2002048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wenheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aecmics-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 33351
LENGTH: 69
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC006160.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.6
OTHER INFORMATION: EXPRESSED IN HB1100, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 2.1

OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.8e+02
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 0.82
OTHER INFORMATION: EST HUMAN HIT: BE168080.1, EVALUATE 4.00e-04
OTHER INFORMATION: SWISSPROT HIT: P25386, EVALUATE 2.00e-03
US-09-864-761-33351

Query Match 69.6%; Score 32; DB 10; Length 69;
Best Local Similarity 87.5%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cy 2 LKSDLVYRK 9
Db 34 LKQDLVYRK 41

RESULT 9
US-09-815-242-12433
Sequence 12433, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Treawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.01A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12433
LENGTH: 117
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12433

Query Match 69.6%; Score 32; DB 10; Length 117;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Cy 1 KXKSQLVYRK 10
Db 105 KLRQGVYRK 114

RESULT 10
US-09-815-242-12867
Sequence 12867, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.

```
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,911
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12867
LENGTH: 117
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-12867
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Query Match          69.6%; Score 32; DB 10; Length 117;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 KLSQVYRK 10
    |||:|:|
Db 105 KLKKELEK 114
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RESULT 11
US-09-815-242-13094
Sequence 13094, Application US/09815242
Patent No. US20020061569A1
GENERAL INFORMATION:
APPLICANT: Hagelbeck, Robert
APPLICANT: Ohlsen, Karl L.
APPLICANT: Zykkind, Judith W.
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John D.
APPLICANT: Carr, Grant J.
APPLICANT: Yamamoto, Robert T.
APPLICANT: Xu, H. Howard
TITLE OF INVENTION: Identification of Essential Genes in
FILE REFERENCE: ELITRA.011A
CURRENT APPLICATION NUMBER: US/09/815,242
CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,911
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
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NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13094
LENGTH: 117
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-815-242-13094
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Query Match          69.6%; Score 32; DB 10; Length 117;
Best Local Similarity 70.0%; Pred. No. 23;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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QY 1 KLSQVYRK 10
    |||:|:|
Db 105 KLKKELEK 114
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RESULT 12
US-09-789-561-191
Sequence 191, Application US/09789561
Patent No. US20020064818A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: 52 Human secreted proteins
FILE REFERENCE: P2043P1
CURRENT APPLICATION NUMBER: US/09/789,561
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/US00/24008
PRIOR FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 60/152,317
PRIOR FILING DATE: 1999-09-03
PRIOR APPLICATION NUMBER: 60/152,315
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 191
LENGTH: 142
TYPE: PRT
ORGANISM: Homo sapiens
US-09-789-561-191
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Query Match          69.6%; Score 32; DB 10; Length 142;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY 1 KLSQVYRK 10
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Db 52 KLSRLTRRK 61
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RESULT 13
US-09-729-674-158
Sequence 158, Application US/09729674
Patent No. US20010039353A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Werberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Agostino, Michael J.
APPLICANT: Steininger II, Robert J.
APPLICANT: Spaulding, Vikki
APPLICANT: Wong, Gordon G.
APPLICANT: Clark, Hilary
APPLICANT: Fachel, Kim
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYPEPTIDES ENCODING THEM
FILE REFERENCE: 6055-64X
CURRENT APPLICATION NUMBER: US/09/729,674
CURRENT FILING DATE: 2000-12-04
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PRIOR APPLICATION NUMBER: 09/539,330
PRIOR FILING DATE: 2000-03-30
NUMBER OF SEQ ID NOS: 283
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 158
LENGTH: 586
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: (286)
US-09-729-674-158

Query Match 69.6%; Score 32; DB 10; Length 586;
Best Local Similarity 60.0%; Pred. No. 1.2e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLKSQLVRRK 10
DB 125 KLRSLRTRRK 134

RESULT 14
US-10-029-009-11
Sequence 11, Application US/10029009
Patent No. US20020164617A1
GENERAL INFORMATION:
APPLICANT: Felisch, Jason S.
APPLICANT: Annis, David Allen
APPLICANT: Kalghatgi, Krishna
APPLICANT: Nash, Huw M.
TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins
FILE REFERENCE: 111025.173 US2
CURRENT APPLICATION NUMBER: US/10/029,009
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 608
TYPE: PRT
ORGANISM: Rat
US-10-029-009-11

Query Match 69.6%; Score 32; DB 9; Length 608;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLKSQLVRRK 10
DB 469 KTRSQITRRK 478

RESULT 15
US-10-029-009-23
Sequence 23, Application US/10029009
Patent No. US20020164617A1
GENERAL INFORMATION:
APPLICANT: Felisch, Jason S.
APPLICANT: Annis, David Allen
APPLICANT: Kalghatgi, Krishna
APPLICANT: Nash, Huw M.
TITLE OF INVENTION: Affinity Selection-Based Screening of Hydrophobic Proteins
FILE REFERENCE: 111025.173 US2
CURRENT APPLICATION NUMBER: US/10/029,009
CURRENT FILING DATE: 2002-03-28
PRIOR APPLICATION NUMBER: US 60/258,970
PRIOR FILING DATE: 2000-12-29
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 23
LENGTH: 626

TYPE: PRT
ORGANISM: Rat
US-10-029-009-23

Query Match 69.6%; Score 32; DB 9; Length 626;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLKSQLVRRK 10
DB 485 KTRSQITRRK 494

Search completed: February 8, 2003, 10:52:11
Job time : 9 secs

GenCore version 5.1.3
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OM protein - protein search, using SW model

Run on: February 8, 2003, 10:41:05 ; Search time 133 Seconds
(Without alignments)
48.476 Million cell updates/sec

Title: US-09-685-010-31

Perfect score: 46

Sequence: 1 KXKSQVKKR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues

Total number of hits satisfying chosen parameters: 4569144

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	46	100.0	10	23	US-09-685-010-31
3	46	100.0	10	23	US-09-978-309A-31
4	43	93.5	10	7	US-08-318-892B-4
5	43	93.5	10	15	US-09-169-077-2
6	43	93.5	10	18	US-09-424-292-6

7	43	93.5	10	18	US-09-424-292-15	Sequence 15, Appl
8	43	93.5	10	18	US-09-424-292-28	Sequence 28, Appl
9	43	93.5	11	7	US-08-318-892-10	Sequence 10, Appl
10	43	93.5	11	7	US-08-318-892B-10	Sequence 10, Appl
11	43	93.5	11	20	US-09-685-010-24	Sequence 24, Appl
12	43	93.5	11	23	US-09-978-309A-24	Sequence 24, Appl
13	43	93.5	32	20	US-09-685-010-51	Sequence 51, Appl
14	43	93.5	32	23	US-09-978-309A-51	Sequence 51, Appl
15	43	93.5	32	23	US-09-978-309A-82	Sequence 82, Appl
16	43	93.5	221	23	US-09-978-309A-75	Sequence 75, Appl
17	43	93.5	333	23	US-09-978-309A-73	Sequence 73, Appl
18	43	93.5	428	7	US-08-318-892B-33	Sequence 33, Appl
19	43	93.5	435	23	US-09-978-309A-80	Sequence 80, Appl
20	43	93.5	476	7	US-08-318-892-2	Sequence 2, Appl
21	43	93.5	476	21	US-09-791-537-42360	Sequence 42360, A
22	43	93.5	476	23	US-09-978-309A-77	Sequence 77, Appl
23	43	93.5	476	23	US-09-978-309A-79	Sequence 79, Appl
24	43	93.5	477	7	US-08-318-892B-2	Sequence 2, Appl
25	43	93.5	477	21	US-09-791-537-88053	Sequence 88053, A
26	43	93.5	606	21	US-09-791-537-67341	Sequence 67341, A
27	43	93.5	630	15	US-09-169-077-6	Sequence 6, Appl
28	43	93.5	631	20	US-09-685-010-48	Sequence 48, Appl
29	43	93.5	631	23	US-09-978-309A-48	Sequence 48, Appl
30	43	93.5	794	21	US-09-791-537-22235	Sequence 22235, A
31	39	84.8	10	15	US-09-169-077-8	Sequence 8, Appl
32	39	84.8	713	24	US-10-023-634-81	Sequence 81, Appl
33	38	82.6	9	20	US-08-318-892B-32	Sequence 32, Appl
34	38	82.6	9	20	US-09-685-010-59	Sequence 59, Appl
35	38	82.6	7	23	US-09-978-309A-59	Sequence 59, Appl
36	38	82.6	10	7	US-08-318-892-13	Sequence 13, Appl
37	38	82.6	10	7	US-08-318-892B-13	Sequence 13, Appl
38	38	82.6	10	18	US-09-424-292-23	Sequence 23, Appl
39	38	82.6	10	18	US-09-424-292-30	Sequence 30, Appl
40	38	82.6	10	18	US-09-424-292-32	Sequence 32, Appl
41	38	82.6	105	21	US-09-733-088-8891	Sequence 8891, Ap
42	38	82.6	103	25	US-09-816-660-8991	Sequence 8991, Ap
43	38	82.6	175	22	US-10-155-881-33553	Sequence 33553, A
44	38	82.6	188	27	US-60-312-544-8435	Sequence 8435, Ap
45	38	82.6	216	19	US-09-563-582-54	Sequence 54, Appl

ALIGNMENTS

RESULT 1
US-08-318-892-4 Application US/08318892
GENERAL INFORMATION:
APPLICANT: Turley, Eva A
TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR
TITLE OF INVENTION: FOR HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318, 892
FILING DATE: 1-DEC-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pieriti, Margaret A
REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIM-8

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-892-4

Query Match          100.0%; Score 46; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLSQLVKRK 10
Db 1 KLSQLVKRK 10

RESULT 2
US-09-685-010-31
; Sequence 31, Application US/09685010
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: CELLULAR RESPONSE TO INJURY AND OTHER PROLIFERATING CELL
; TITLE OF INVENTION: DISORDERS REGULATED BY HYALADHERIN AND HYALURONANS
; FILE REFERENCE: 910130.401C1
; CURRENT APPLICATION NUMBER: US/09/685.010
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide composition that binds a hyalauronan
US-09-685-010-31

Query Match          100.0%; Score 46; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLSQLVKRK 10
Db 1 KLSQLVKRK 10

RESULT 3
US-09-978-309A-31
; Sequence 31, Application US/09978309A
; GENERAL INFORMATION:
; APPLICANT: Cruz, Tony
; APPLICANT: Pasitrek, Aleksandra
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
; FILE REFERENCE: 033352-010
; CURRENT APPLICATION NUMBER: US/09/978.309A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 09/685.010
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/541,522
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/127,457
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide composition that binds a hyalauronan
US-09-978-309A-31

Query Match          100.0%; Score 46; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLSQLVKRK 10
Db 1 KLSQLVKRK 10

RESULT 4
US-08-318-892B-4
; Sequence 4, Application US/08318892B
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR FOR
; TITLE OF INVENTION: HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING PEPTIDES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,892B
; FILING DATE: 1-DEC-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pierri, Margaret A
; REGISTRATION NUMBER: 30709
; REFERENCE/DOCKET NUMBER: SIM-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9090
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-892B-4

Query Match          93.5%; Score 43; DB 7; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLSQLVKRK 10
Db 1 KLSQLVKRK 10

RESULT 5
US-09-169-077-2
; Sequence 2, Application US/09169077
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN HYALURONAN RECEPTOR
; NUMBER OF SEQUENCES: 52
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/169,077
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/CA97/00240
FILING DATE:
APPLICATION NUMBER: GB 9607441.4
FILING DATE: 10-APR-1996
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-169-077-2

Query Match 93.5%; Score 43; DB 15; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLRSQLVYRK 10
Db 1 KLRSQLVYRK 10

RESULT 6
US-09-424-292-6
Sequence 6, Application US/09424292
GENERAL INFORMATION:
APPLICANT: Turley, Eva A
TITLE OF INVENTION: Improved Delivery of Disease Modifiers
FILE REFERENCE: 205375
CURRENT APPLICATION NUMBER: US/09/424,292
CURRENT FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: PCT/CA98/00448
PRIOR FILING DATE: 1998-05-11
PRIOR APPLICATION NUMBER: CA 2,205,771
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 6
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-424-292-6

Query Match 93.5%; Score 43; DB 18; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLRSQLVYRK 10
Db 1 KLRSQLVYRK 10

RESULT 7
US-09-424-292-15
Sequence 15, Application US/09424292
GENERAL INFORMATION:
APPLICANT: Turley, Eva A
TITLE OF INVENTION: Improved Delivery of Disease Modifiers
FILE REFERENCE: 205375
CURRENT APPLICATION NUMBER: US/09/424,292
CURRENT FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: PCT/CA98/00448

PRIOR FILING DATE: 1998-05-11
PRIOR APPLICATION NUMBER: CA 2,205,771
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-424-292-15

Query Match 93.5%; Score 43; DB 18; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLRSQLVYRK 10
Db 1 KLRSQLVYRK 10

RESULT 8
US-09-424-292-28
Sequence 28, Application US/09424292
GENERAL INFORMATION:
APPLICANT: Turley, Eva A
TITLE OF INVENTION: Improved Delivery of Disease Modifiers
FILE REFERENCE: 205375
CURRENT APPLICATION NUMBER: US/09/424,292
CURRENT FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: PCT/CA98/00448
PRIOR FILING DATE: 1998-05-11
PRIOR APPLICATION NUMBER: CA 2,205,771
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 28
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-424-292-28

Query Match 93.5%; Score 43; DB 18; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLRSQLVYRK 10
Db 1 KLRSQLVYRK 10

RESULT 9
US-08-318-892-10
Sequence 10, Application US/08318892
GENERAL INFORMATION:
APPLICANT: Turley, Eva A
TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR
TITLE OF INVENTION: FOR HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,892
FILING DATE: 1-DEC-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pierri, Margaret A
REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIM-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-892-10

Query Match 93.5%; Score 43; DB 7; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.47;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLKSQLVKKR 10
Db 2 KLKSQLVKKR 11

RESULT 10
US-08-318-892B-10
Sequence 10, Application US/08318892B
GENERAL INFORMATION:

APPLICANT: Turley, Eva A
TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR FOR
TITLE OF INVENTION: HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING PEPTIDES
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: c/o FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,892B
FILING DATE: 1-DEC-1994
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pierri, Margaret A
REGISTRATION NUMBER: 30709
REFERENCE/DOCKET NUMBER: SIM-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 596-9000
TELEFAX: (212) 596-9090
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-892B-10

Query Match 93.5%; Score 43; DB 7; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.47;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 KLKSQLVKKR 10
Db 2 KLKSQLVKKR 11

RESULT 11
US-09-685-010-24
Sequence 24, Application US/09685010
GENERAL INFORMATION:
APPLICANT: Turley, Eva A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
CELLULAR RESPONSE TO INJURY AND OTHER PROLIFERATING CELL
TITLE OF INVENTION: DISORDERS REGULATED BY HYALADHERIN AND HYALURONANS
FILE REFERENCE: 910130.401C1
CURRENT APPLICATION NUMBER: US/09/685,010
CURRENT FILING DATE: 2001-05-23
NUMBER OF SEQ ID NOS: 72
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapien
US-09-685-010-24

Query Match 93.5%; Score 43; DB 20; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.47;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLKSQLVKKR 10
Db 1 KLKSQLVKKR 10

RESULT 12
US-09-978-309A-24
Sequence 24, Application US/09978309A
GENERAL INFORMATION:
APPLICANT: Cruz, Tony
APPLICANT: Pastrak, Aleksandra
TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
TITLE OF INVENTION: Hyaladerin and Hyaluronans
FILE REFERENCE: 03352-010
CURRENT APPLICATION NUMBER: US/09/978,309A
CURRENT FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 09/685,010
PRIOR FILING DATE: 2000-10-05
PRIOR APPLICATION NUMBER: US 09/541,522
PRIOR FILING DATE: 2000-04-03
PRIOR APPLICATION NUMBER: US 60/127,457
PRIOR FILING DATE: 1999-04-01
NUMBER OF SEQ ID NOS: 84
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapien
US-09-978-309A-24

Query Match 93.5%; Score 43; DB 23; Length 11;
Best Local Similarity 90.0%; Pred. No. 0.47;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLKSQLVKKR 10
Db 1 KLKSQLVKKR 10

RESULT 13

```

US-09-685-010-51
; Sequence 51, Application US/09685010
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A.
; APPLICANT: Cruz, Tony F.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: CELLULAR RESPONSE TO INJURY AND OTHER PROLIFERATING CELL
; FILE REFERENCE: 910130,401C1
; CURRENT APPLICATION NUMBER: US/09/685,010
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Peptide used in competition binding assay
US-09-685-010-51

```

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Query Match          93.5%; Score 43; DB 20; Length 32;
Best Local Similarity 90.0%; Pred. No. 1.6;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KLRKSQLVYRK 10
   ||:|||||
Db 23 KLRKSQLVYRK 32

```

```

RESULT 14
US-09-978-309A-51
; Sequence 51, Application US/0978309A
; GENERAL INFORMATION:
; APPLICANT: Cruz, Tony
; APPLICANT: Pasttrak, Aleksandra
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
; FILE REFERENCE: 033352-010
; CURRENT APPLICATION NUMBER: US/09/978,309A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 09/685,010
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/541,522
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/127,457
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 51
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Peptide used in competition binding assay
US-09-978-309A-51

```

```

Query Match          93.5%; Score 43; DB 23; Length 32;
Best Local Similarity 90.0%; Pred. No. 1.6;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KLRKSQLVYRK 10
   ||:|||||
Db 23 KLRKSQLVYRK 32

```

```

RESULT 15
US-09-978-309A-82
; Sequence 82, Application US/09978309A
; GENERAL INFORMATION:
; APPLICANT: Cruz, Tony

```

```

; APPLICANT: Pasttrak, Aleksandra
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
; FILE REFERENCE: 033352-010
; CURRENT APPLICATION NUMBER: US/09/978,309A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 09/685,010
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/541,522
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/127,457
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 82
; LENGTH: 32
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-978-309A-82

```

```

Query Match          93.5%; Score 43; DB 23; Length 32;
Best Local Similarity 90.0%; Pred. No. 1.6;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 1 KLRKSQLVYRK 10
   ||:|||||
Db 23 KLRKSQLVYRK 32

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Search completed: February 8, 2003, 10:50:49
Job time : 133 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:41:35 ; Search time 15 Seconds
(without alignments)
54.053 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KLSQVLKRR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 405691 seqs, 81078759 residues

Total number of hits satisfying chosen parameters: 405691

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending_Patents_AA_New:*
1: /cgn2_6/ptodata/2/paa/PCT_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	38	82.6	242	US-10-310-154-439	Sequence 439, App
2	36	78.3	544	US-60-434-832-7073	Sequence 7073, App
3	35	76.1	190	US-10-017-161-1700	Sequence 1700, App
4	34	73.9	188	US-10-294-025-592	Sequence 592, App
5	33	71.7	627	US-10-284-060-28	Sequence 28, App
6	33	71.7	627	US-10-284-060-28	Sequence 28, App
7	33	71.7	627	US-10-284-060-28	Sequence 28, App
8	33	71.7	1190	US-10-284-060-26	Sequence 26, App
9	33	71.7	1190	US-10-284-060-26	Sequence 26, App
10	33	71.7	1190	US-10-284-060-26	Sequence 26, App
11	32	69.6	99	US-10-203-138A-10373	Sequence 10373, A
12	32	69.6	99	US-09-724-676A-49554	Sequence 49554, A
13	32	69.6	99	US-09-724-676A-49554	Sequence 49554, A
14	32	69.6	100	US-10-264-237-1662	Sequence 1662, App
15	32	69.6	119	US-09-950-084-5149	Sequence 5149, App
16	32	69.6	153	US-09-724-676A-49560	Sequence 49560, A
17	32	69.6	153	US-09-724-676A-49560	Sequence 49560, A
18	32	69.6	249	US-09-724-676A-49550	Sequence 49550, A
19	32	69.6	249	US-09-724-676A-49550	Sequence 49550, A
20	32	69.6	303	US-09-724-676A-49563	Sequence 49563, A
21	32	69.6	303	US-09-724-676A-49563	Sequence 49563, A
22	32	69.6	417	US-09-134-000C-5144	Sequence 5144, App
23	32	69.6	417	US-09-134-000C-5144	Sequence 5144, App
24	32	69.6	590	US-10-161-916A-5	Sequence 5, App
25	31	67.4	66	US-10-092-411A-3095	Sequence 3095, App
26	31	67.4	69	US-10-092-411A-4988	Sequence 4988, App

27	30	65.2	217	5	US-09-134-000C-4232	Sequence 4232, App
28	30	65.2	217	5	US-09-134-000C-4232	Sequence 4232, App
29	30	65.2	288	5	US-09-950-084-4086	Sequence 4086, App
30	30	65.2	328	6	US-10-295-403-80	Sequence 80, App
31	30	65.2	393	6	US-10-329-624-5248	Sequence 5248, App
32	30	65.2	489	6	US-10-310-154-181	Sequence 381, App
33	30	65.2	502	6	US-10-017-161-2042	Sequence 2042, App
34	30	65.2	2434	6	US-10-218-140-4056	Sequence 4056, App
35	29	63.0	82	1	PCT-US02-3727-11254	Sequence 11254, A
36	29	63.0	82	6	US-10-057-498-11254	Sequence 11254, A
37	29	63.0	180	6	US-10-218-140-3928	Sequence 3928, App
38	29	63.0	194	5	US-09-134-000C-6648	Sequence 6648, App
39	29	63.0	194	5	US-09-134-000C-6648	Sequence 6648, App
40	29	63.0	243	6	US-10-310-154-635	Sequence 635, App
41	29	63.0	247	6	US-10-310-154-639	Sequence 639, App
42	29	63.0	324	5	US-09-950-084-6446	Sequence 6446, App
43	29	63.0	411	5	US-09-724-676-61733	Sequence 61733, A
44	29	63.0	411	5	US-09-724-676-61734	Sequence 61734, A
45	29	63.0	411	5	US-09-724-676A-61733	Sequence 61733, A

ALIGNMENTS

RESULT 1
US-10-310-154-439
Sequence 439, Application US/10310154
GENERAL INFORMATION:
APPLICANT: Edgerton, Michael D
APPLICANT: Chomet, Paul S.
APPLICANT: Adams, Thomas H
APPLICANT: Ruff, Thomas G.
APPLICANT: Agarwal, Ameeta K.
APPLICANT: Ahrens, Jeffrey E.
APPLICANT: Ball, James A.
APPLICANT: Banu, G.
APPLICANT: Bell, Erin
APPLICANT: Boddupalli, Raghava
APPLICANT: Deikman, Jill
APPLICANT: Deng, Molian
APPLICANT: Dong, Jinhua
APPLICANT: Duff, Stephen M.
APPLICANT: Galligan, Meghan M.
APPLICANT: Hinchey, Brenda S.
APPLICANT: Huang, Shihshieh
APPLICANT: Johnson, G. Richard
APPLICANT: Jung, Vincent
APPLICANT: Kretzmer, Keith A.
APPLICANT: Lacetelli, Lucille B.
APPLICANT: Lai, Chao-Qiang
APPLICANT: Lee, Gary
APPLICANT: Lin, Jie-Yi
APPLICANT: Liu, Jindong
APPLICANT: Lu, Bin
APPLICANT: Luehly, Michael M.
APPLICANT: Lund, Adrian
APPLICANT: Madison, Linda L.
APPLICANT: Malloy, Kathleen A.
APPLICANT: McKiel, Christine U.
APPLICANT: Miller, Philip W.
APPLICANT: Padmavathi, Manoharant
APPLICANT: Parnell, Laurence D.
APPLICANT: Scarf, William G.
APPLICANT: Teneesen, Dan
APPLICANT: Vidya, K.R.
APPLICANT: Wang, Haiyun
APPLICANT: Xin, Zhanguo
APPLICANT: Xu, Nanfei
APPLICANT: Yang, Chunzhi
APPLICANT: Zeng, Xiaoping
APPLICANT: Zhang, Qiang
APPLICANT: Zhou, Yajuan
APPLICANT: Zhou, Li

;; TITLE OF INVENTION: Gene Sequences and Uses Thereof in Plants
;; FILE REFERENCE: 38-15(52796)B
;; CURRENT APPLICATION NUMBER: US/10/310,154
;; CURRENT FILING DATE: 2002-12-04
;; PRIOR APPLICATION NUMBER: 60/337,358
;; PRIOR FILING DATE: 2001-12-04
;; NUMBER OF SEQ ID NOS: 736
;; SEQ ID NO 439
;; LENGTH: 242
;; TYPE: PRT
;; ORGANISM: Zea mays
US-10-310-154-439

Query Match 82.6%; Score 38; DB 6; Length 242;
Best Local Similarity 80.0%; Pred. No. 1.7;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 LKSQLVKKR 10
|||:|
Db 136 LKSHLKKR 145

RESULT 2
US-60-434-832-7073
; Sequence 7073, Application US/60434832
; GENERAL INFORMATION:
; APPLICANT: Roemer, Terry
; APPLICANT: Jiang, Bo
; APPLICANT: Boone, Charles
; APPLICANT: Busey, Howard
; TITLE OF INVENTION: Nucleic Acids Encoding Antifungal Drug Targets and Methods of Use
; FILE REFERENCE: 10182-023-888
; CURRENT APPLICATION NUMBER: US/60/434,832
; CURRENT FILING DATE: 2002-12-19
; NUMBER OF SEQ ID NOS: 7137
; SOFTWARE: Patent version 3.1
; SEQ ID NO 7073
; LENGTH: 544
; TYPE: PRT
; ORGANISM: Candida albicans
US-60-434-832-7073

Query Match 78.3%; Score 36; DB 7; Length 544;
Best Local Similarity 88.9%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 LKSQLVKKR 10
|||:|
Db 245 LNSQLVKKR 253

RESULT 3
US-10-017-161-1700
; Sequence 1700, Application US/10017161
; GENERAL INFORMATION:
; APPLICANT: SUMA, MAKIKO
; APPLICANT: ASAI, KIYOSHI
; APPLICANT: AKIYAMA, YUTAKA
; APPLICANT: ABUDATANI, HIROYUKI
; TITLE OF INVENTION: NOVEL G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 084335/0152
; CURRENT APPLICATION NUMBER: US/10/017,161
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: JP 2001/246789
; PRIOR FILING DATE: 2001-06-18
; NUMBER OF SEQ ID NOS: 2430
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1700
; LENGTH: 190
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-161-1700

Query Match 76.1%; Score 35; DB 6; Length 190;
Best Local Similarity 60.0%; Pred. No. 5.6;
Matches 6; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 1 LKSQLVKKR 10
|||:|
Db 169 LKSQLKKR 178

RESULT 4
US-10-294-025-592
; Sequence 592, Application US/10294025
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Stolk, John A.
; APPLICANT: Kaios, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.427C29
; CURRENT APPLICATION NUMBER: US/10/294,025
; CURRENT FILING DATE: 2002-11-12
; NUMBER OF SEQ ID NOS: 1038
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 592
; LENGTH: 188
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-294-025-592

Query Match 73.9%; Score 34; DB 6; Length 188;
Best Local Similarity 77.8%; Pred. No. 9;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 LKSQLVKKR 10
|||:|
Db 178 LKSQLKKR 186

RESULT 5
US-10-284-060-28
; Sequence 28, Application US/10284060
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: French-Constant, Richard
; APPLICANT: Orr, Gregory L
; APPLICANT: Merlo, Donald J
; APPLICANT: Roberts, Jean L
; APPLICANT: Rocheleau, Thomas A
; TITLE OF INVENTION: Insecticidal Protein Toxins from
; TITLE OF INVENTION: Photorhabdus
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Dowelanco
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/284,060
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/063,615

FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/743,699
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50301E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-284-060-28

Query Match 71.7%; Score 33; DB 6; Length 627;
Best Local Similarity 70.0%; Pred. No. 57;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KXKSQLVWRK 10
|||:|:|
Db 146 KXKSELVRSK 155

RESULT 6
US-10-284-060-28
; Sequence 28, Application US/10284060
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: French-Constant, Richard
; APPLICANT: Orr, Gregory L
; APPLICANT: Merlo, Donald J
; APPLICANT: Roberts, Jean L
; APPLICANT: Rochelleau, Thomas A
; TITLE OF INVENTION: Insecticidal Protein Toxins from
; TITLE OF INVENTION: Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowelanco
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/284,060
; FILING DATE:
; CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/743,699
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50301E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-284-060-28

Query Match 71.7%; Score 33; DB 6; Length 627;
Best Local Similarity 70.0%; Pred. No. 57;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KXKSQLVWRK 10
|||:|:|
Db 146 KXKSELVRSK 155

RESULT 7
US-10-284-060-28
; Sequence 28, Application US/10284060
; GENERAL INFORMATION:
; APPLICANT: Ensign, Jerald C
; APPLICANT: Bowen, David J
; APPLICANT: Petell, James
; APPLICANT: Fatig, Raymond
; APPLICANT: Schoonover, Sue
; APPLICANT: French-Constant, Richard
; APPLICANT: Orr, Gregory L
; APPLICANT: Merlo, Donald J
; APPLICANT: Roberts, Jean L
; APPLICANT: Rochelleau, Thomas A
; TITLE OF INVENTION: Insecticidal Protein Toxins from
; TITLE OF INVENTION: Photorhabdus
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dowelanco
; STREET: 9330 Zionsville Road
; CITY: Indianapolis
; STATE: IN
; COUNTRY: US
; ZIP: 46268
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/284,060

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/743,699
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50301E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 627 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-284-060-28

Query Match 71.7%; Score 33; DB 6; Length 627;
Best Local Similarity 70.0%; Pred. No. 57;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KXKSQLVKRX 10
Db 146 KXKSQLVKRX 155

RESULT 8
US-10-284-060-26
Sequence 26, Application US/10284060
GENERAL INFORMATION:
APPLICANT: Ensign, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Fatig, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: French-Constant, Richard
APPLICANT: Orr, Gregory L
APPLICANT: Merlo, Donald J
APPLICANT: Roberts, Jean L
APPLICANT: Rochelleau, Thomas A
TITLE OF INVENTION: Insecticidal Protein Toxins from
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelanco
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,060
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/743,699
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50301E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-284-060-26

Query Match 71.7%; Score 33; DB 6; Length 1190;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KXKSQLVKRX 10
Db 146 KXKSQLVKRX 155

RESULT 9
US-10-284-060-26
Sequence 26, Application US/10284060
GENERAL INFORMATION:
APPLICANT: Ensign, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Fatig, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: French-Constant, Richard
APPLICANT: Orr, Gregory L
APPLICANT: Merlo, Donald J
APPLICANT: Roberts, Jean L
APPLICANT: Rochelleau, Thomas A
TITLE OF INVENTION: Insecticidal Protein Toxins from
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowelanco
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,060
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/743,699
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50301E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-284-060-26

Query Match 71.7%; Score 33; DB 6; Length 1190;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KXKSQVYRK 10
Db 146 KXKSELVESK 155

RESULT 10
US-10-284-060-26
Sequence 26, Application US/10284060
GENERAL INFORMATION:
APPLICANT: Ensign, Jerald C
APPLICANT: Bowen, David J
APPLICANT: Petell, James
APPLICANT: Fatid, Raymond
APPLICANT: Schoonover, Sue
APPLICANT: French-Constant, Richard
APPLICANT: Orr, Gregory L
APPLICANT: Merlo, Donald J
APPLICANT: Roberts, Jean L
APPLICANT: Rochelleau, Thomas A
TITLE OF INVENTION: Insecticidal Protein Toxins from
TITLE OF INVENTION: Photorhabdus
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dowlancco
STREET: 9330 Zionsville Road
CITY: Indianapolis
STATE: IN
COUNTRY: US
ZIP: 46268
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/284,060
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/063,615
FILING DATE: 18-MAY-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/395,497
FILING DATE: 28-FEB-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/007,255
FILING DATE: 06-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/608,423
FILING DATE: 28-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/705,484
FILING DATE: 28-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/743,699
FILING DATE: 06-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Borucki, Andrea T.
REGISTRATION NUMBER: 33651
REFERENCE/DOCKET NUMBER: 50301E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 317-337-4846
TELEFAX: 317-337-4847
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 1189 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-10-284-060-26

Query Match 71.7%; Score 33; DB 6; Length 1190;
Best Local Similarity 70.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KXKSQVYRK 10
Db 146 KXKSELVESK 155

RESULT 11
US-10-203-138A-10373
Sequence 10373, Application US/10203138A
GENERAL INFORMATION:
APPLICANT: Molecular Dynamics, Inc.
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
TITLE OF INVENTION: ANALYSIS OF GENE EXPRESSION IN BT 474
FILE REFERENCE: PB 0004 WO 8
CURRENT APPLICATION NUMBER: US/10/203,138A
CURRENT FILING DATE: 2002-08-02
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 04 February 2000 (04.02.00)
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 26 May 2000 (26.05.00)
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 03 August 2000 (03.08.00)
PRIOR APPLICATION NUMBER: GB 24263,6
PRIOR FILING DATE: 03 October 2000 (03.10.00)
PRIOR APPLICATION NUMBER: US 60/236,359

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/ PRIOR FILING DATE: 27 September 2000 (27.09.00)
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 21 September 2000 (21.09.00)
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 30 June 2000 (30.06.00)
/ NUMBER OF SEQ ID NOS: 15438
/ SOFTWARE: Molecular Dynamics Sequence Listing Engine
/ SEQ ID NO 10373
/ LENGTH: 69
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC006160.9
/ FEATURE:
/ OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.1
/ FEATURE:
/ OTHER INFORMATION: EST_HUMAN HIT: B6168080.1, EVALUE 4.00e-04
/ FEATURE:
/ OTHER INFORMATION: SWISSPROT HIT: P25386, EVALUE 2.00e-03
/ US-10-203-138A-10373
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Query Match          69.6%; Score 32; DB 6; Length 69;
Best Local Similarity 87.5%; Pred. No. 7.7;
Matches 7; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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QY      2 LKSQLVKK 9
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Db      34 LKQQLVKK 41
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RESULT 12
US-09-724-676-49554
/ Sequence 49554, Application US/09724676
/ GENERAL INFORMATION:
/ APPLICANT: Compugen LTD
/ TITLE OF INVENTION: Variants of alternative splicing
/ FILE REFERENCE: 129181.4 Compugen
/ CURRENT APPLICATION NUMBER: US/09/724,676
/ CURRENT FILING DATE: 2000-11-28
/ NUMBER OF SEQ ID NOS: 97222
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 49554
/ LENGTH: 99
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-724-676-49554
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Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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QY      1 KLSQLVKK 10
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Db      62 KLRQVKKR 71
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RESULT 13
US-09-724-676A-49554
/ Sequence 49554, Application US/09724676A
/ GENERAL INFORMATION:
/ APPLICANT: Compugen LTD
/ TITLE OF INVENTION: Variants of alternative splicing
/ FILE REFERENCE: 129181.4 Compugen
/ CURRENT APPLICATION NUMBER: US/09/724,676A
/ CURRENT FILING DATE: 2000-11-28
/ NUMBER OF SEQ ID NOS: 97222
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 49554
/ LENGTH: 99
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-09-724-676A-49554
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Query Match          69.6%; Score 32; DB 5; Length 99;
Best Local Similarity 60.0%; Pred. No. 12;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
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```
QY      1 KLSQLVKK 10
      ||| |||
Db      62 KLRQVKKR 71
```

```
RESULT 14
US-10-264-237-1662
/ Sequence 1662, Application US/10264237
/ GENERAL INFORMATION:
/ APPLICANT: Birse et al.
/ TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
/ FILE REFERENCE: P4131P
/ CURRENT APPLICATION NUMBER: US/10/264,237
/ CURRENT FILING DATE: 2002-10-04
/ PRIOR APPLICATION NUMBER: PCT/US01/16450
/ PRIOR FILING DATE: 2001-05-18
/ PRIOR APPLICATION NUMBER: US 60/205,515
/ PRIOR FILING DATE: 2000-05-19
/ NUMBER OF SEQ ID NOS: 2876
/ SOFTWARE: PatentIn Ver. 3.1
/ SEQ ID NO 1662
/ LENGTH: 100
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-264-237-1662
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```
Query Match          69.6%; Score 32; DB 6; Length 100;
Best Local Similarity 77.8%; Pred. No. 12;
Matches 7; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY      2 LKSQLVKK 10
      ||| |||
Db      38 LKQQLVKK 46
```

```
RESULT 15
US-09-950-084-5149
/ Sequence 5149, Application US/09950084
/ GENERAL INFORMATION:
/ APPLICANT: George H. Shimer, Jr.
/ APPLICANT: George H. Miller
/ APPLICANT: Roberta S. Hare
/ APPLICANT: Karen J. Shaw
/ TITLE OF INVENTION: Staphylococcus aureus Related Compositions and Methods
/ FILE REFERENCE: 1034/IC963US2
/ CURRENT APPLICATION NUMBER: US/09/950,084
/ CURRENT FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: US 09/417,811
/ PRIOR FILING DATE: 1999-10-14
/ PRIOR APPLICATION NUMBER: US 09/353,718
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: US 09/266,557
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 09/266,556
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 09/266,555
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 09/266,542
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 09/266,541
/ PRIOR FILING DATE: 1999-03-11
/ PRIOR APPLICATION NUMBER: US 09/037,934
/ PRIOR FILING DATE: 1998-03-10
/ PRIOR APPLICATION NUMBER: US 09/036,720
/ PRIOR FILING DATE: 1998-03-06
/ PRIOR APPLICATION NUMBER: US 09/036,338
/ PRIOR FILING DATE: 1998-03-06
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 7451
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; SEQ ID NO 5149
; LENGTH: 119
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-950-084-5149

Query Match 69.6%; Score 32; DB 5; Length 119;
Best Local Similarity 70.0%; Pred. No. 14;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXKSQLVKRK 10
Db 107 KXKXKXKXK 116

Search completed: February 8, 2003, 10:51:43
Job time : 16 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:39:30 ; Search time 11.3333 Seconds
(without alignments)
25.961 Million cell updates/sec

Title: US-09-685-010-31

Perfect score: 46

Sequence: 1 KLRSQLVVRK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	93.5	32	4	US-08-477-831C-38
2	43	93.5	477	1	US-08-402-217A-3
3	43	93.5	477	1	US-08-700-178-3
4	43	93.5	477	3	US-08-995-654-3
5	43	93.5	606	4	US-08-477-831C-2
6	43	93.5	631	4	US-08-477-831C-11
7	35	76.1	316	3	US-08-801-344-4
8	35	76.1	316	3	US-09-498-599-4
9	34	73.9	188	4	US-09-605-785-592
10	32	69.6	18	1	US-07-725-331-32
11	32	69.6	18	5	PCT-US91-05047-32
12	32	69.6	316	1	US-08-585-585-3
13	32	69.6	355	1	US-08-118-270-11
14	32	69.6	355	5	PCT-US93-08528-11
15	31	67.4	66	4	US-09-134-001C-3095
16	31	67.4	69	4	US-09-134-001C-4988
17	31	67.4	166	3	US-08-765-381-6
18	31	67.4	294	4	US-09-103-664A-5
19	31	67.4	351	1	US-08-402-217A-2
20	31	67.4	351	1	US-08-700-178-2
21	31	67.4	351	4	US-08-995-654-2
22	31	67.4	534	4	US-09-103-664A-2
23	29	65.2	3169	4	US-09-453-702B-257
24	29	63.0	479	1	US-08-313-553-7
25	29	63.0	479	3	US-08-767-993-7
26	29	63.0	1493	4	US-09-376-330-16
27	29	63.0	2089	1	US-08-418-893D-23

28	29	63.0	2089	1	US-08-418-893D-24	Sequence 24, Appl
29	29	63.0	3165	2	US-08-459-146-3	Sequence 3, Appl
30	29	63.0	3165	2	US-08-459-065-3	Sequence 3, Appl
31	28	60.9	28	1	US-08-427-072-13	Sequence 13, Appl
32	28	60.9	32	4	US-08-477-831C-39	Sequence 39, Appl
33	28	60.9	42	1	US-08-062-872B-26	Sequence 26, Appl
34	28	60.9	42	4	US-09-122-171D-8	Sequence 8, Appl
35	28	60.9	48	3	US-08-460-890A-49	Sequence 49, Appl
36	28	60.9	48	3	US-08-167-641C-49	Sequence 49, Appl
37	28	60.9	48	4	US-08-460-971A-49	Sequence 49, Appl
38	28	60.9	48	4	US-08-462-040-49	Sequence 49, Appl
39	28	60.9	49	2	US-08-460-890A-48	Sequence 48, Appl
40	28	60.9	49	3	US-08-167-641C-48	Sequence 48, Appl
41	28	60.9	49	4	US-08-460-971A-48	Sequence 48, Appl
42	28	60.9	49	4	US-08-462-040-48	Sequence 48, Appl
43	28	60.9	52	1	US-08-309-419-7	Sequence 7, Appl
44	28	60.9	52	1	US-08-309-419-7	Sequence 7, Appl
45	28	60.9	52	5	PCT-US95-11856-7	Sequence 7, Appl

ALIGNMENTS

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RESULT 1
US-08-477-831C-38
; Sequence 38, Application US/08477831C
; Patent No. 6429291
GENERAL INFORMATION:
; APPLICANT: TURLEY, EVA A.
; APPLICANT: SHWEN, ZHANG
; APPLICANT: ENTWISTLE, JOYCELYN
; TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
; NUMBER OF SEQUENCES: 60
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FISH & NEAVE
; STREET: 1251 AVENUE OF THE AMERICAS
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: U.S.A.
; ZIP: 10020-1104
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Rel. #1.0, ASCII
CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,831C
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: PIERRE, MARGARET A.
; REGISTRATION NUMBER: 30,709
; REFERENCE/DOCKET NUMBER: SIM-10
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 38:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: /desc = protein fragment
; DESCRIPTION: /desc = protein fragment
; US-08-477-831C-38

Query Match 93.5%; Score 43; DB 4; Length 32;
Best Local Similarity 90.0%; Pred. No. 0.17;
Matches 9; Conservative 1; Mismatches 0; Gaps 0;
Indels 0;
QY 1 KLRSQLVVRK 10
||:|||||
Db 23 KLRSQLVVRK 32
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RESULT 2
US-08-402-217A-3
; Sequence 3, Application US/08402217A
; Patent No. 5587301
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
; TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/402,217A
; FILING DATE: 10-MAR-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Luther, Barbara J.
; REGISTRATION NUMBER: 33954
; REFERENCE/DOCKET NUMBER: PF-00280US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-0195
; TELEFAX: 415-852-0195
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 477 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; IMMEDIATE SOURCE:
; LIBRARY: mouse
; CLONE: GI 53979
US-08-402-217A-3

Query Match 93.5%; Score 43; DB 1; Length 477;
Best Local Similarity 90.0%; Pred. No. 2.1;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KLSQLVKRX 10
||:|||||
Db 424 KLRSQLVKRX 433

RESULT 3
US-08-700-178-3
; Sequence 3, Application US/08700178
; Patent No. 5783669
; Patent No. 5783669 5700912
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig G.
; APPLICANT: Seilhamer, Jeffrey J.
; TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
; TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 Porter Drive
; CITY: Palo Alto

STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/700,178
FILING DATE: August 20, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/402,217
FILING DATE: March 10, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0028-1 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-845-4166
TELEFAX: 415-845-0555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
IMMEDIATE SOURCE:
LIBRARY: mouse
CLONE: GI 53979
US-08-700-178-3

Query Match 93.5%; Score 43; DB 1; Length 477;
Best Local Similarity 90.0%; Pred. No. 2.1;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Cy 1 KLSQLVKRX 10
||:|||||
Db 424 KLRSQLVKRX 433

RESULT 4
US-08-995-654-3
; Sequence 3, Application US/08995654
; Patent No. 6025138
; GENERAL INFORMATION:
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Wilde, Craig
; APPLICANT: Seilhamer, Jeffrey
; TITLE OF INVENTION: HYALURONAN RECEPTOR EXPRESSED IN HUMAN
; TITLE OF INVENTION: UMBILICAL VEIN ENDOTHELIAL CELLS
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Dr.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/995,654
; FILING DATE: December 22, 1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/700,178
; FILING DATE: August 20, 1996

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/402,217
FILING DATE: March 10, 1995
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PP-0028-2 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 477 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-995-654-3

Query Match 93.5%; Score 43; DB 3; Length 477;
Best Local Similarity 90.0%; Pred. No. 2.1;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLSQVYRK 10
||:|||||
Db 424 KLSQVYRK 433

RESULT 5
US-08-477-831C-2
Sequence 2, Application US/08477831C
Patent No. 6429291
GENERAL INFORMATION:
APPLICANT: TURLEY, EVA A.
APPLICANT: SHUMEN, ZHANG
APPLICANT: ENTWISTLE, JOYCELYN
TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10020-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Rel. #1.0, ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477, 831C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PIERRE, MARGARET A.
REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIM-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 606 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: /desc = "RHAMM I protein"
US-08-477-831C-2

Query Match 93.5%; Score 43; DB 4; Length 606;
Best Local Similarity 90.0%; Pred. No. 2.6;

Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KLSQVYRK 10
||:|||||
Db 553 KLSQVYRK 562

RESULT 6
US-08-477-831C-11
Sequence 11, Application US/08477831C
Patent No. 6429291
GENERAL INFORMATION:
APPLICANT: TURLEY, EVA A.
APPLICANT: SHUMEN, ZHANG
APPLICANT: ENTWISTLE, JOYCELYN
TITLE OF INVENTION: HYALURONAN RECEPTOR PROTEIN
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 AVENUE OF THE AMERICAS
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10020-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Rel. #1.0, ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477, 831C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: PIERRE, MARGARET A.
REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIM-10
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9090
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 631 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: /desc = "RHAMM I-2a"
US-08-477-831C-11

Query Match 93.5%; Score 43; DB 4; Length 631;
Best Local Similarity 90.0%; Pred. No. 2.7;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLSQVYRK 10
||:|||||
Db 578 KLSQVYRK 587

RESULT 7
US-08-801-344-4
Sequence 4, Application US/08801344
Patent No. 6087140
GENERAL INFORMATION:
APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim B.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL
TITLE OF INVENTION: FROM SUGAR
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Demilt Ross & Stevens S.C.
STREET: 8000 Excelsior Drive, Suite 401

CITY: Madison
STATE: WI
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/801,344
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100
FAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHEITICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat lens aldose reductase
US-08-801-344-4

Query Match 76.1%; Score 35; DB 3; Length 316;
Best Local Similarity 70.0%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LKSQLVKK 10
|||:||||:
Db 62 LKKEQVKKQ 71

RESULT 8
US-09-498-599-4
Sequence 4, Application US/09498599
Patent No. 6303352
GENERAL INFORMATION:
APPLICANT: Cameron, Douglas C.
APPLICANT: Shaw, Anita J.
APPLICANT: Altaras, Nedim B.
TITLE OF INVENTION: MICROBIAL PRODUCTION OF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: WI
COUNTRY: U.S.A.
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,599
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REFERENCE/DOCKET NUMBER: 09820.037
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-831-2100

TELEFAX: 608-831-2106
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 316 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Protein
HYPOTHEITICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Rat lens aldose reductase
US-09-498-599-4

Query Match 76.1%; Score 35; DB 4; Length 316;
Best Local Similarity 70.0%; Pred. No. 38;
Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 LKSQLVKK 10
|||:||||:
Db 62 LKKEQVKKQ 71

RESULT 9
US-09-605-785-592
Sequence 592, Application US/09605785
Patent No. 6321716
GENERAL INFORMATION:
APPLICANT: Xu, Jiangchun
APPLICANT: Dillon, Devin C.
APPLICANT: Mitcham, Jennifer L.
APPLICANT: Harlocker, Susan L.
APPLICANT: Jiang, Yuqi
APPLICANT: Henderson, Robert A.
APPLICANT: Kalos, Michael D.
APPLICANT: Fanger, Gary R.
APPLICANT: Retter, Marc W.
APPLICANT: Stoik, John A.
APPLICANT: Day, Craig H.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Derrick
APPLICANT: Li, Samuel
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Hepler, William
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
FILE REFERENCE: 210121.427C16
CURRENT APPLICATION NUMBER: US/09/605,785
CURRENT FILING DATE: 2000-06-27
NUMBER OF SEQ ID NOS: 835
SOFTWARE: PasteSeq for Windows Version 3.0
SEQ ID NO 592
LENGTH: 188
TYPE: PRT
ORGANISM: Homo sapien
US-09-605-785-592

Query Match 73.9%; Score 34; DB 4; Length 188;
Best Local Similarity 77.8%; Pred. No. 35;
Matches 7; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LKSQLVKK 10
|||:||||:
Db 178 LKAQLVKK 186

RESULT 10
US-07-725-331-32
Sequence 32, Application US/07725331
Patent No. 5294605
GENERAL INFORMATION:
APPLICANT: Houghten, Richard

APPLICANT: Blondelle, Sylvie
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sucker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 No. 5294605th Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/725,331
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165418
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: C-terminal amide, acetylated at
US-07-725-331-32

Query Match 69.6%; Score 32; DB 1; Length 18;
Best Local Similarity 60.0%; Pred. No. 8.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKKSQLVRRK 10
Db 2 KKKKKLKKK 11

RESULT 11
PCT-US91-05047-32
Sequence 32, Application PC/TUS9105047
GENERAL INFORMATION:
APPLICANT: Houghten, Richard
TITLE OF INVENTION: Amphiphilic Peptide Compositions and
TITLE OF INVENTION: Analogues Thereof
NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Goldsmith, Sucker, Shore,
ADDRESSEE: & Milnamow
STREET: 180 North Stetson
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05047
FILING DATE: 19910717
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/554,422
FILING DATE: 19-JUL-1990
ATTORNEY/AGENT INFORMATION:
NAME: Gamsen, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: 421250-80
TELECOMMUNICATION INFORMATION:
TELEPHONE: 3126165418
TELEFAX: 3126165418
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
OTHER INFORMATION: C-terminal amide, acetylated at
US-09-685-010-31-32

Query Match 69.6%; Score 32; DB 5; Length 18;
Best Local Similarity 60.0%; Pred. No. 8.9;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KKKSQLVRRK 10
Db 2 KKKKKLKKK 11

RESULT 12
US-08-585-595-3
Sequence 3, Application US/08585595
Patent No. 5795761
GENERAL INFORMATION:
APPLICANT: POWERS, DAVID B.
TITLE OF INVENTION: IMPROVED METHODS FOR PRODUCING VITAMIN C
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: HOWREY & SIMON
STREET: 1299 PENNSYLVANIA AVENUE, N.W.
CITY: WASHINGTON
STATE: DC
COUNTRY: US
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,595
FILING DATE: 16-JAN-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/584,019
FILING DATE: 11-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: AUERBACH, JEFFREY I.
REGISTRATION NUMBER: 32680
REFERENCE/DOCKET NUMBER: 6137-0014 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 383-7451
TELEFAX: (202) 383-6610
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:

LENGTH: 316 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: ADPOSE REDUCTASE
STRAIN: HOMO SAPIENS
US-08-585-595-3

Query Match 69.6%; Score 32; DB 1; Length 316;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KXKSQLVKK 10
Db 62 KLRQVKKRE 71

RESULT 13

US-08-118-270-11
Sequence 11, Application US/08118270
Patent No. 5508384

GENERAL INFORMATION:
APPLICANT: Murphy, Randall B.
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/118,270
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-118-270-11

Query Match 69.6%; Score 32; DB 1; Length 355;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXKSQLVKK 10
Db 236 KTRSQITKRX 245

RESULT 14
PCT-US93-08528-11
Sequence 11, Application PC/TUS9308528

GENERAL INFORMATION:
APPLICANT: New York University
TITLE OF INVENTION: POLYPEPTIDES OF G-COUPLED PROTEIN
TITLE OF INVENTION: RECEPTORS, AND COMPOSITIONS AND METHODS THEREOF
NUMBER OF SEQUENCES: 348
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/08528
FILING DATE: 09-SEP-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/943,236
FILING DATE: 10-SEP-1992
ATTORNEY/AGENT INFORMATION:
NAME: Townsend, Kevin G.
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: MURPHY=2 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 355 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-08528-11

Query Match 69.6%; Score 32; DB 5; Length 355;
Best Local Similarity 60.0%; Pred. No. 1.4e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 KXKSQLVKK 10
Db 236 KTRSQITKRX 245

RESULT 15
US-09-134-001C-3095
Sequence 3095, Application US/09134001C

GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: EPIDERMIDS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR FILING DATE: 1997-08-14
NUMBER OF SEQ ID NOS: 5674
SEQ ID NO 3095

LENGTH: 66
TYPE: PRT
ORGANISM: Staphylococcus epidermidis
US-09-134-001C-3095

Query Match 67.4%; Score 31; DB 4; Length 66;
Best Local Similarity 66.7%; Pred. No. 45;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 KTKSQLYKR 9
|:|:|:|
Db 5 KTKSLIKR 13

Search completed: February 8, 2003, 10:44:05
Job time : 12.333 secs

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0|0 Intelligenetics
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Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq28-pen" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence.

Selected sequence key from "new.key":
seq28 (AA) ID seq28 AA preliminary pattern

1 followed by

2 \$

2 r or k or h

2 a or r or n or c or g or g or h or i or l or k or m or f or p or s or t or w

2 r or k or h

2 end of scope

Selected data banks and files:

Data bank : Pending_AA , all entries

-- Output Parameters --

Format Options:

Nucleic acid code matching Exact

Find non-matching hits only No

Report key used Yes

Note position of hit Yes

Display full annotations Yes

Sequence context 10

File Options:

Indirect file

Sequence or key file

List of hits

Hit display

Name and annotations

No
No
No
Yes
Yes
Yes

-- Run Parameters --

Run mode

Time to start comparison

Notify at end of run

Batch
now
No

No hits found.

-- Search Statistics --

Times:

CPU
00:20:25.06

Total Elapsed
00:22:42.00

Number of sequences searched:

496936

Number of sequence hits:

0

Number of separate matches:

0

Number of sequence hits saved:

0

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O | | O Intelligenetics
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Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq28-1ss" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence.

Selected sequence key from "new.key":

seq28 (AA) ID seq28 AA preliminary pattern
followed by

1 \$
2 r or k or h
2 a or r or n or c or g or h or i or l or k or m or f or p or s or t or w
2 r or k or h
2 end of scope

Selected data banks and files:

Data bank : Issued_AA , all entries

-- Output Parameters --

Format Options:

Nucleic acid code matching	Exact	File Options:	
Find non-matching hits only	No	Indirect file	No
Report key used	Yes	Sequence or key file	No
Note position of hit	Yes	List of hits	No
Display full annotations	Yes	Hit display	Yes
Sequence context	10	Name and annotations	Yes

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

No hits found.

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:01:10.06	00:01:11.00
Number of sequences searched:		262643
Number of sequence hits:		0
Number of separate matches:		0
Number of sequence hits saved:		0

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> O <
O | | O Intelligenetics
> O <

Quest - Quick User-directed Expression Search Tool
Release 5.4

-- Outline of search "seq28-wpat" --

Selected search type is key against sequence data banks or files.

Selected scope is Sequence.

Selected sequence key from "new.key":

seq28 (AA) ID seq28 AA preliminary pattern
followed by

1 \$
2 r or k or h
2 a or r or n or c or g or h or l or k or m or f or p or s or t or w
2 r or k or h
2 end of scope

Selected data banks and files:

Data bank : A-Geneseq 35.2, all entries

-- Output Parameters --

Format Options:

Nucleic acid code matching	Exact	File Options:	
Find non-matching hits only	No	Indirect file	No
Report key used	Yes	Sequence or key file	No
Note position of hit	Yes	List of hits	No
Display full annotations	Yes	Hit display	Yes
Sequence context	10	Name and annotations	Yes

-- Run Parameters --

Run mode	Batch
Time to start comparison	now
Notify at end of run	No

No hits found.

-- Search Statistics --

Times:	CPU	Total Elapsed
	00:00:18.07	00:00:22.00
Number of sequences searched:		170751
Number of sequence hits:		0
Number of separate matches:		0
Number of sequence hits saved:		0

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! FINDPATTERNS on genpept:* allowing 0 mismatches
!
! 1 <(R,K,H) (A,R,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V) {7,7} (R,K,H) >
!
! CAA00584 ck: 3637 len: 9 ! GB:A06625 D11 carboxy-terminus [synthetic c
!
! <(R,K,H) (A,R,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V) {7,7} (R,K,H) >
! (K) (I,L,T,Y,V) {7} (R)
! KLIYILTVR
!
! CAA01163 ck: 3637 len: 9 ! GB:A14468 unnamed protein product [Fowl]pox
!
! <(R,K,H) (A,R,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V) {7,7} (R,K,H) >
! (K) (I,L,T,Y,V) {7} (R)
! KLIYILTVR
!
! AAM50387 ck: 3482 len: 9 ! GB:AF384615 ribosomal protein 16 [Howlttia
!
! <(R,K,H) (A,R,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V) {7,7} (R,K,H) >
! (K) (R,Q,K,P,T) {7} (H)
! KRTRFRKQH
!
! AAB22067 ck: 3653 len: 9 ! GB:S95530 zinc finger protein [Homo sapiens]
!
! <(R,K,H) (A,R,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V) {7,7} (R,K,H) >
! (R) (N,Q,I,T,Y,V) {7} (K)
! RNOVTIYTK
!
! CAA24737 ck: 3472 len: 9 ! GB:V01492 bradykinin [Bos taurus] (ver 1)
!
! <(R,K,H) (A,R,N,C,Q,G,H,I,L,K,M,F,P,S,T,W,Y,V) {7,7} (R,K,H) >
! (R) (G,F,P,S) {7} (R)
! RPPGFSPFR
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Databases searched:

GENPEPT, Release 131.0, Released on 30Aug2002, Formatted on 31Aug2002

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Total finds: 5
Total length: 348,344,575
Total sequences: 1,135,942
CPU time: 03:51.14
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!!SEQUENCE LIST 1.0
! FINDPATTERNS on genpept:* allowing 0 mismatches
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GP:CAA00584      ck: 3637  len: 9      finds: 1      ! GB:A06625 D11 carboxy-terminus
GP:CAA01163      ck: 3637  len: 9      finds: 1      ! GB:A14468 unnamed protein prod
GP:AAM50387      ck: 3482  len: 9      finds: 1      ! GB:AF384615 ribosomal protein
GP:AAB22067      ck: 3653  len: 9      finds: 1      ! GB:S95530 zinc finger protein
GP:CAA24737      ck: 3472  len: 9      finds: 1      ! GB:V01492 bradykinin [Bos tau]

\\End of list

Databases searched:
GENPEPT, Release 131.0, Released on 30Aug2002, Formatted on 31Aug2002

Total finds: 5
Total lengths: 348,344,575
Total sequences: 1,135,942
CPU time: 05:55.83

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!!AA_SEQUENCE 1.0
CAA01163 GB:A14468 unnamed protein product [Fowlpox virus] (ver 1)
CAA01163 Length: 9 February 11, 2003 12:16 Type: P Check: 3637 ..
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!!AA_SEQUENCE 1.0
AAM50387 GB:AF384615 ribosomal protein 16 [Howittia trilocularis] (ver 1)
AAM50387 Length: 9 February 11, 2003 12:16 Type: P Check: 3482 ..
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AAB22067 GB:S95530 zinc finger protein [Homo sapiens] (ver 1)
AAB22067 Length: 9 February 11, 2003 12:16 Type: P Check: 3653 ..
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!!AA_SEQUENCE 1.0
CAA24737 GB:V01492 bradykinin [Bos taurus] (ver 1)
CAA24737 Length: 9 February 11, 2003 12:16 Type: P Check: 3472 ..
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!INA_SEQUENCE 1.0
LOCUS       A06625                2681 bp    DNA             linear    PAT 30-JUN-1993
DEFINITION  Synthetic nucleotide sequence of the FPV, including the genes D7,
            D8 and D10.
ACCESSION   A06625
VERSION     A06625.1
KEYWORDS    GI:412913
SOURCE      synthetic construct.
            SOURCE      synthetic construct
            ORGANISM    artificial sequences.
FEATURES             location/Qualifiers
     source          1..2681
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                     /note="D7 carboxy-terminus"
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                     /gene="D8"
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                     /NEVSTPRSRVMDSDGRPIKTECAFSTRRIYGRSOUNIKMKIKDIGITRKRCQTSQV
                     /NLLHTYGGISLSIPNPTGSGTCKMVCVTGCGIGNVGRFLVKSLSPLSDTESDHS
                     /YTSRSGHPMECKVKSPYGMIVE"
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51 AAAAAATATA CTTTAATAA GATTAATTA CATATAACT ACATCATGTA
101 AGGTATAGCT TATTAACAT GGATAGCAT TATTAATATT TGTAAATCA
151 AAAAACTACT TAAATATTTT AATAGTATAT TGAATTCCTT ATCAGTAGA
201 AAGATATTAG TTATACACAC AATGATATGT AAAAAATGTA TTCGACATTA
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251 AGAATTGACG TTGATTAAT TTTCTGCTT TATATATCTA TCAAAACTT
301 TTGTAGAAGT AAAAGCACT CCTATGTAC TGTACCGGA AGTAGTGATA
351 TAAATCTTAC TTGTTTATT AAAGATGATC AGGTGCTGG AGAAGATTA
401 GTAAATTGAG CGTGACACA GGGTGACGGA GAAGTTACTC AAGAAATAA
451 AACAACTTGG GATACGACAC GACAAGTGG CCAACCAATG CTACATATAT
501 CCAAGTATC TAAAGAACCA GAAGTTTCAI AATATGTCT TGTATGATA
551 AACGCGACG CTGATTATTA AAAATGAAT CTAGAGTGT TTACTGTTTC
601 AAAAAAACCC TACATGCATA ACGAAGTAA TTAACCCCT CGAAGATGA
651 GAGTAGATAT GTCGATGCT CGGCCGCTTA AATTAATG TGCTTTTATG
701 ACCCGACGAA TATATGTTAG AAGCCAAATC AACATTAAT GTGGAAGAT
751 TGACCGTATC ACAGAAAT GGGAAACA CACTTCGGGA GTTAACCTAC
801 TGTTCATAC TTATGAGGG ATAGATCGC TAAGTATCCC AAATCCTACA
851 ACAGAGAAT CAACAGTAA GTATATGTC GTAGTTACCT GTGAGATAT
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951 CAGAACTGTA TCATAGTTAT ACTTCAGAGG AAGATCACA TTTTATGGA
1001 AGATCCAAAG TCAAAAAAG TCCGTACGCT GGATGATAG TAGAATAGAT
1051 CATTCAGAGG ACGGGGATA TATTGCTATA AGTAAATA ATTCTCAAT
1101 ACATTTTCT ACTTAAACA TATATCGTT AACTATTAG TTTAATTATA
1151 TCATATATTC CTTTATATCT TAATTAAAA AATATATTC TAAATGGAT
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1251 GTTTATCAAA CATAGTGAA AATTAACAA CTATAAAAA TAAGATCATG
1301 TTGATATAT CCAGAACAA ACAAAATATA TTAGAAAAA ATAAAGATTG
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1551 ATAAACCATC TAAATATAT GTATTAATAC GAAATTAAG AATATATCAT
1601 AATCAATAG TACCATCAC ATATAGCGA TTCACAAC TGAAGAGTT
1651 AGTATTATTA GGAGAGAGG TTAATAATA AGAATCAATA TATCAATGCC
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1751 TTTGTAATA AAATATTA ACTTACCATA GAAGATTAAG TACTTCGTAG
1801 AATATTTTAT GGTATTTGTA TAGTGTTT TATAGACCA CTCATTCAG
1851 AATCATTAAC ACCTTATAT AACATAGAA TCAAGAAAT AGGATCATTA
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2001 CTAGGCGCT CTGATATTC TGATTAATA CAAAAATCA AACTGTAGC
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2151 TTCTTGTTTT CAGAAATAGC ATTACAAA GATAAGGAC GGAATAAAG
2201 ACTCTTAAG AATATTCAA AGTATATGAG TAACATGAA CGTGATATAT
2251 TAAGTATATA GCTATGCTT CCTAATACT ATAAATACAA CCATATAGAT
2301 ATATCTTCC CAGGTGTAA AATAAAGAC TTGAAAGTA TAACTAATTG
2351 TCTAGTAA GAAATAAAG AAGATTAA TATGATTCC TCTTATCTCG
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2501 TAGACAATA TTGAATAGAT TCATCCCTTA TAGAATAATT AAGGAATAT
2551 CATTATAGA CGCAGAGAT ATTACAAAG ATTATTGTA TACTAATGTA
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2651 TCTATCTAAC TGTTAATATA TAAATTAATT T

!INA_SEQUENCE 1.0
LOCUS A14468 2681 bp DNA linear PAT 06-JUL-1995
DEFINITION Carboxy-terminus.
ACCESSION A14468
VERSION A14468.1 GI:492962
KEYWORDS
SOURCE Fowlpox virus.
ORGANISM Fowlpox virus
Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
Avipoxvirus.
REFERENCE 1 (bases 1 to 2681)
AUTHORS Bims,M.K., Bournell,M.E.G., Campbell,J.I.A. and Tomley,F.M.
TITLE Fowlpox virus non-essential regions
JOURNAL Patent: EP 0353851-A 7 07-FEB-1990;
NATIONAL RESEARCH DEVELOPMENT CORPORATION
FEATURES
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488..1048
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CDS complement(2652..2681)
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/note="unnamed protein product"
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/translation="KLIIYLTVR"
BASE COUNT 1072 a 354 c 428 g 827 t
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A14468 Length: 2681 February 11, 2003 15:09 Type: N Check: 6533

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251 AGAATTGACG TTGATTAATAT TTCTTGCTT TATATATCTA TCAAAAACCT
301 TTGTAGAAAT AAAAGCACCT CCTATGTAC TCGTACCGGA AGTAGTGATA
351 TAAATCTTAC TTGTTTATTT AAAGATGATC AGGGTGCTGG AGAAGATATA
401 GTAATTGTAG CGTGCAACA GGGTGACGGA GAAGTTACTC AAGGAATATA
451 AACAACTTG GATACGACAC GACAGTGGG CCAACCAAG CTACATATAT
501 CCAAGGTATC TAAAGAACCA GAAGTTTCAT ATATGTGTGT TGTATGATA
551 AACGGCAGC CTGATTATTA AAAAATGAAT CTAGAGTGT TTACTGTTTC
601 AAAAAAACCC TACATGCATA ACGAATGAG TATTAACCCCT CGAAGATGGA
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701 ACCCGACGAA TATATGGTAG AAGCCAAGTC AACATTAAT GGTGGAAAGAT
751 TGACGGTATC ACAGAAAT GGAACAACA GACTCGGGA GTTAACCTTAC
801 TGTTACATAC TTATGAGAGG ATAGATCGC TAAGTATCCC AAATCCTTACA
851 ACAGGAGAAAT CAACAGTTA GTATATGTGC GTAGTTACCT GTGAGATAT
901 TGAATAATGT GGAATTAGAC TGGTAAATC ATTATCTCCT TTATCAGATA
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2201 ACTCTTAAG AATATTCA AGTATATGAG TAACATCGA CGTATATAT
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!!NA_SEQUENCE 1.0
LOCUS AF384615 1138 bp DNA linear PLN 11-JUN-2002
DEFINITION Howittia trilobularis ribosomal protein 16 (rpl16) gene, intron and
partial cds; chloroplast gene for chloroplast product.
ACCESSION AF384615
VERSION AF384615.1 GI:21388904
KEYWORDS
SOURCE
ORGANISM Howittia trilobularis.
Chloroplast Howittia trilobularis
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Malvales; Malvaceae; Howittia.
REFERENCE
AUTHORS Pfeil,B.E., Brubaker,C.L., Craven,L.A. and Crisp,M.D.
TITLE Phylogeny of Hibiscus and the tribe Hibisceae (Malvaceae) using
JOURNAL chloroplast DNA sequences of ndhF and the rpl16 intron
SYST. BOT. 27 (2), 333-350 (2002)
2 (bases 1 to 1138)
Pfeil,B.E., Brubaker,C.L., Craven,L.A. and Crisp,M.D.
Direct Submission
JOURNAL Submitted (23-MAY-2001) Center for Plant Biodiversity Research,
CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia
FEATURES
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CDS
intron
BASE COUNT 468 a 156 c 178 g 336 t
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AF384615 Length: 1138 February 11, 2003 15:09 Type: N Check: 849 ..
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51 ACTATAGCAC TAATACCA CTCAATCGCT CGGATTATCT GGATCCAAAG
101 AATCACTCAA GATATGATAT ATTGTCATA TCATTATAGC AACTGAATTT
151 TTTTGGCAT TAAGTAAAG AAAAACCAG TCGATTAGG AATATATCTA
201 AATTGTGAAG CAAATTAATA AATATGTGA TAAATAGAAG GATGAGAGAA
251 AGAGAGAAAA AGAATAGCA ATGAATGAT ATATGATTCC AATATGTAAG
301 GTCTATGAAG CATTCATTA AGACCAATGT AATAGAGCAT CAATAGAGAT
351 TCATCAAGAA ATCAATTAAT AGATGAATAT CTGTTCAATG AAAAAAAT
401 CAAGACCTTT AACTTAAGTC AATTAAGACT GAGAAGGTG ACTCAAGAAC
451 AATTTTATT TAATTTTTT TATTAATTA AATATTTAA ACGAAGCTC
501 CATTTAGAA TTCAGACCTA AGCATTAATC GAGAAGGAT GGGAGCAGC
551 GAACCCGTGA ATGCAAGAT TCTATTGAA ACGAATCCTA ATGATTTATC
601 GGGTAGAGTG GGGGAACAAA CCGAGACCA CTTCATTCTT TTTTATTTG
651 ATTCTGAGAG GTTATGAGTT AACCGACAA CTGAACCTAGA TATGAAAGA

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701 GTAAATATTC GCCCGCGAAA ATTTAATTTT CATTTAAT TTATTGATT
751 GTTAATTTT TGTGANTCG AATCTGATAT GAATATGATA AAAACAAAA
801 TTAAGATTTC TTATACATT ATACAAAAC CAAGTAAAG CATATCTAG
851 AATGAATTC CGTGTTAAT TACTATATA TATATCAAT ATATATCCA
901 ACAAGATATA CAAATTTCTA ATAGATCAGA TAAATATCA AAGCAAGAA
951 TCCCAAGATT CAATCTATTA TTCAATTAAT ACTGTATAT CTTAAGATA
1001 AATAGTTT TTAGTCATTT TTTTTCGGG AGAAGCTGGA TGAAGAAGAA
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!!NA_SEQUENCE 1.0
LOCUS BTXIN2 3174 bp mRNA linear MAM 12-SEP-1993
DEFINITION Bovine messenger RNA coding for kininogen (clone pKG203). This
gives rise to bradykinin a vasoactive peptide.
ACCESSION V01492 K01758
VERSION V01492.1 GI:493
KEYWORDS bradykinin; complementary DNA; kininogen.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
1 (bases 1 to 3174)
Kitamura, N., Takagaki, Y., Furuto, S., Tanaka, T., Nawa, H. and
Nakanishi, S.
TITLE A single gene for bovine high molecular weight and low molecular
weight kininogens
JOURNAL Nature 305 (5934), 545-549 (1983)
MEDLINE 84014106
PUBMED 6571699
COMMENT Data kindly reviewed (05-FEB-1984) by N. Kitamura.
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1 A43065 ck: 3472 len: 9 1 hydroxyproline-3-bradykinin - frog (Helleoph
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PIR2:A60579      ck: 3478 len: 9      finds: 1      ! bradykinin-like peptide - slid
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C:Accession: A61057
R:Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.
Comp. Biochem. Physiol. C 96, 157-162, 1990
A:Title: Theonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.)
presynaptically blocks nicotinic synaptic transmission in the insect CNS.
A:Reference number: A61057; MUID:91130217; PMID:1980872
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C>Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 18-Aug-2000
C:Accession: A26744
R:Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
Toxicol 25, 527-535, 1987
A:Title: Two kinins isolated from an extract of the venom reservoirs of the
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A:Reference number: A94322; MUID:87293024; PMID:3617088
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A26744 Length: 9 February 11, 2003 12:15 Type: P Check: 3478 ..

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R:Anastasi, A.; Erspamer, V.; Bertaccini, G.
Comp. Biochem. Physiol. A 14, 43-52, 1965
A:Title: Occurrence of bradykinin in the skin of Rana temporaria.
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C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 18-Aug-2000
C:Accession: A60579
R:Conlon, U.M.; Hicks, J.W.; Smith, D.D.
Endocrinology 126, 985-991, 1990
A:Title: Isolation and biological activity of a novel kinin
(Thr(6))bradykinin) from the turtle, Pseudemys scripta.
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1 RPPGFPPR

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C:Accession: B60246
R:Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.
Adv. Exp. Med. Biol. 247A, 359-367, 1989
A:Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and
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A:Reference number: A60246; MUID:90102072; PMID:2603803
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C:Accession: S65433
R:Wijffels, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.;
Willadsen, P.
Eur. J. Biochem. 237, 414-423, 1996
A:Title: Cloning and characterisation of angiotensin-converting enzyme from the
dipteran species, Haematobia irritans exigua, and its expression in the
maturing male reproductive system.
A:Reference number: S65433; MUID:96215437; PMID:8647080
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S65433 Length: 9 February 11, 2003 12:15 Type: P Check: 3472 ..

1 RPPGFPPR

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C>Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-May-1999
C:Accession: A43065
R:Nakajima, T.; Yasuhara, T.; Erspamer, G.F.; Vassier, J.
Experientia 35, 1133, 1979
A:Title: Occurrence of Hyp(3)-bradykinin in methanol extracts of the skin of
the South African leopodactylid frog Heleophryne purcellii.
A:Reference number: A43065; MUID:80024576; PMID:488255
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A43065 Length: 9 February 11, 2003 12:15 Type: P Check: 3472 ..

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1: (R) (G,F,P,S) {7} (R)
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1 P83059 ck: 3478 len: 9 1 P83059 bombina orientalis (oriental fire-ba
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Databases searched:

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SPTRMBL, Release 21.0, Released on 15Jun2002, Formatted on 28Jun2002

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SP_OV:P83060      ck: 3472 len: 9   finds: 1   ! P83060 bombina orientalis (ori
SP_OV:P83059      ck: 3478 len: 9   finds: 1   ! P83059 bombina orientalis (ori
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Databases searched:
  SWISS-PROT, Release 40.3, Released on 9Aug2002, Formatted on 20Aug2002
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DE BRADYKININ.
OS Lepisosteus osseus (long-nosed gar), and
OS Amla calva (Bowfin).
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RP MEDLINE=95380361; PubMed=7651903;
RA Conlon J.M., Platzack B., Marra L.E., Youson J.H., Olson K.R.;
RT "Isolation and biological activity of [Trp5]bradykinin from the plasma
RT of the phylogenetically ancient fish, the bowfin and the longnosed
RT gar.";
RL Peptides 16:485-489 (1995).
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RC TISSUE=SKIN SECRETION;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
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KM Vasodilator; Bradykinin.
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OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
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AC_P83058;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Bradykinin-like peptide ([Thr6]bradykinin).
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxId=8348;
RN [1]
RP TISSUE=SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=SKIN SECRETION;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: SKIN.
SQ_SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;
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P83058 Length: 9 February 11, 2003 12:16 Type: P Check: 3478 ..

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1 RPPGTPFR
!!AA_SEQUENCE 1.0
ID_P83056 PRELIMINARY; PRT; 9 AA.
AC_P83056;
DT 01-OCT-2001 (TREMBlrel. 18, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)
DE Bradykinin-like peptide ([Ila3,Thr6]bradykinin).
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxId=8348;
RN [1]
RP TISSUE=SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RC TISSUE=SKIN SECRETION;
RA Chen T.B., Orr D.F., Bjourson A.J., McClean S., Rao P.F., Shaw C.;
RT "Cloning and post-translational processing of frog skin kininogens.";
RL Submitted (JUL-2001) to the SWISS-PROT data bank.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- TISSUE SPECIFICITY: SKIN.
SQ_SEQUENCE 9 AA; 1048 MW; 3393D771A9C87D07 CRC64;
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P83056 Length: 9 February 11, 2003 12:16 Type: P Check: 3433 ..

1 RPPGTPFR

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2003, 10:57:01 ; Search time 14 Seconds
(without alignments)
75.534 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KQKIKHVVKLK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 1326

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_73:***
1: pir1:***
2: pir2:***
3: pir3:***
4: pir4:***

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	21	38.9	7	2	PQ0663
2	21	38.9	11	2	A33917
3	20	37.0	7	2	A28709
4	19	35.2	10	2	S13324
5	17	31.5	6	2	S11024
6	17	31.5	10	2	S43631
7	16	29.6	8	2	T14906
8	16	29.6	10	2	PQ0783
9	16	29.6	11	2	S3519
10	15	27.8	10	2	S56825
11	15	27.8	10	2	S6385
12	14	25.9	6	2	JH0784
13	14	25.9	6	2	S78764
14	14	25.9	7	2	JN0859
15	14	25.9	9	2	A60356
16	14	25.9	9	2	I54379
17	14	25.9	9	2	S78426
18	14	25.9	10	2	A32543
19	14	25.9	10	2	A56633
20	14	25.9	11	2	G42762
21	14	25.9	11	2	S6606
22	14	25.9	11	2	S19301
23	14	25.9	11	2	A61483
24	13	24.1	3	3	A60898
25	13	24.1	7	2	S29735
26	13	24.1	9	2	S55696
27	13	24.1	9	2	I46016
28	13	24.1	9	2	S78762
29	13	24.1	9	2	PC7076

30	13	24.1	9	2	PC7073	ubiquinol-cytochro
31	13	24.1	10	2	C45474	thrombospondin 2 -
32	13	24.1	10	2	S27873	hypothetical prote
33	13	24.1	10	2	S23307	neurokinin A - rat
34	13	24.1	10	2	S23186	neurokinin A - Atl
35	13	24.1	10	2	S09387	pyl protein - huma
36	13	24.1	10	2	PS0451	24k protein 4302 -
37	13	24.1	10	2	A43977	FMRFamide-like pro
38	13	24.1	10	2	A30823	bothropstoxin - ja
39	13	24.1	10	2	I48778	small nuclear ribo
40	13	24.1	10	2	A44871	monodehydroascorba
41	13	24.1	10	2	S74147	glyceroldehyde-3-P
42	13	24.1	11	2	PQ0733	unidentified 6.0/1
43	13	24.1	11	4	I52708	ELAV-like neuronal
44	12	22.2	6	2	S02617	alcohol dehydrogen
45	12	22.2	6	2	S11556	hydrogensulfite re

ALIGNMENTS

RESULT 1
PQ0663
membrane protein - porcine epidemic diarrhea virus (isolate Belgian CV777) (fragment)
C:Species: porcine epidemic diarrhea virus
C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 08-Oct-1999
C:Accession: PQ0663
R:Bridge, A.; Duarte, M.; Tobler, K.; Laude, H.; Ackermann, M.
J. Gen. Virol. 74, 1795-1804, 1993
A:Title: Sequence determination of the nucleocapsid protein gene of the porcine epide
missible gastroenteritis virus.
A:Reference number: JQ2191; MUID:93389433; PMID:8397280
A:Accession: PQ0663
A:Molecule type: mRNA
A:Residues: 1-7

A:Cross-references: GB:214976; NID:9311650; PIDN:CAA78699.1; PID:9584083
C:Comment: This virus is coronavirus related to human coronavirus 229E.
C:Keywords: membrane protein

Query Match 38.9%; Score 21; DB 2; Length 7;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 QKIKHV 8
Db 1 EKVLLV 7

RESULT 2

A33917
dihydroorotase (EC 3.5.2.3) - Chinese hamster (fragment)
C:Species: Cricetus griseus (Chinese hamster)
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 07-Nov-1997
C:Accession: A33917
R:Stimmer, J.P.; Kelly, R.E.; Sully, J.L.; Grayson, D.R.; Rinker Jr., A.G.; Bergh, S.
Proc. Natl. Acad. Sci. U.S.A. 86, 4362-4386, 1989
A:Title: Mammalian aspartate transcarbamylase (ATCase): sequence of the ATCase domain
A:Reference number: A33917; MUID:89282776; PMID:2543974
A:Accession: A33917
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-11 <SIM>
A:Cross-references: A33917; MUID:89282776; PMID:2543974
C:Keywords: hydroxylase

Query Match 38.9%; Score 21; DB 2; Length 11;
Best Local Similarity 37.5%; Pred. No. 9.2e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 QKIKHV 9
|||::

Db 4 OKVKGITR 11

RESULT 3

A:28709
phosphonoacetaldehyde hydrolase - *Bacillus cereus* (fragment)
C:Species: *Bacillus cereus*
C>Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C:Accession: A28709
R:Olson, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988
A>Title: Investigation of the *Bacillus cereus* phosphonoacetaldehyde hydrolase. Evidence
Idue.
A:Reference number: A28709; MUID:88241058; PMID:3132206
A:Accession: A28709
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <OLS>

Query Match 37.0%; Score 20; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHV 7
1 1 1
Db 2 KIDHV 6

RESULT 4

S13224
virC protein - *Agrobacterium* sp. (fragment)
C:Species: *Agrobacterium* sp.
C>Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 01-Aug-1997
C:Accession: S13224
R:Tamamoto, S.; Aoyama, T.; Takamaml, M.; Oka, A.
J. Mol. Biol. 215, 537-547, 1990
A>Title: Binding of the regulatory protein virC to the phased signal sequences upstream
A:Reference number: S13224; MUID:91039316; PMID:2231718
A:Accession: S13224
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <TAM>

Query Match 35.2%; Score 19; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 IKHV 8
1 1 1
Db 1 MKHV 5

RESULT 5

S11024
hydrogensulfite reductase (EC 1.8.99.3) chain 1 - *Desulfovibrio thermophilus* (fragment)
N:Alternate names: disulfite reductase; desulfosulfidase
C:Species: *Desulfovibrio thermophilus*
C>Date: 19-Mar-1997 #sequence_revision 30-Jan-1998 #text_change 30-Jan-1998
C:Accession: S11024
R:Paugue, G.; Lino, A.R.; Czechowski, M.; Kang, L.; DerVartanian, D.V.; Moura, J.J.G.; I
Biochim. Biophys. Acta 1040, 112-118, 1990
A>Title: Purification and characterization of bisulfite reductase (desulfosulfidase) from
A:Reference number: S11024; MUID:90335276; PMID:2165817
A:Accession: S11024
A:Molecule type: protein
A:Residues: 1-6 <FAU>
C:Keywords: oxidoreductase

Query Match 31.5%; Score 17; DB 2; Length 6;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 VVKLV 11

Db 2 IVKFK 6

RESULT 6

S43631
cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, cardiac - rainbow trout (fragment)
C:Species: *Oncorhynchus mykiss* (rainbow trout)
C>Date: 20-Oct-1994 #sequence_revision 01-Nov-1996 #text_change 16-Jul-1999
C:Accession: S43631
R:Freund, R.; Kadenbach, B.
Eur. J. Biochem. 221, 1111-1116, 1994
A>Title: Identification of tissue-specific isoforms for subunits Vb and VIIa of cyto
A:Reference number: S43624; MUID:94237150; PMID:8181469
A:Accession: S43631
A:Molecule type: protein
A:Residues: 1-10 <FRF>
A>Note: the source is designated as *Salmo gairdneri*
C:Keywords: cardiac muscle; heart; membrane-associated complex; mitochondrion; oxidor

Query Match 31.5%; Score 17; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 4.4e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 KOKIKHVKL 10
1 1 1
Db 1 KKKVPPXXOKL 10

RESULT 7

T14906
hypothetical protein - parsley
C:Species: *Petroselinum crispum* (parsley)
C>Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T14906
R:Feildruege, M.; Sprenger, M.; Dinkelbach, M.; Yazaki, K.; Harter, K.; Weisshaar, B.
Plant Cell 6, 1607-1621, 1994
A>Title: Functional analysis of a light-responsive plant bz1p transcriptional regulat
A:Reference number: T14906; MUID:95128172; PMID:7827494
A:Accession: T14906
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-8 <FEU>
A:Cross-references: EMBL:S75395; NID:g913201; PID:e194245

Query Match 29.6%; Score 16; DB 2; Length 8;
Best Local Similarity 28.6%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 4 IKHVKL 10
1 1 1
Db 1 MKHLLTI 7

RESULT 8

P00783
NADH dehydrogenase (EC 1.6.99.3) 30K chain - fava bean mitochondrion (fragment)
N:Alternate names: complex I 30K chain; NADH-ubiquinone reductase 30K chain
C:Species: *mitochondrion Vicia faba* (fava bean)
C>Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 03-Jun-2002
C:Accession: P00783
R:Letierme, S.; Boutry, M.
Plant Physiol. 102, 435-443, 1993
A>Title: Purification and preliminary characterization of mitochondrial complex I (NA
A:Reference number: P00775; MUID:94151437; PMID:8108509
A:Accession: P00783
A:Molecule type: protein
A:Residues: 1-10 <LEU>

Query Match 31.5%; Score 17; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 4.4e+03;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 1 KOKIKHVKL 10

C:Genetics
A:Genome: mitochondrion
C:Keywords: electron transfer; mitochondrion; oxidoreductase

Query Match 29.6%; Score 16; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 6.7e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 KHV 7
||:
Db 6 KHI 8

RESULT 9

S33519
probable secreted protein - *Acholeplasma laidlawii* (fragment)

C:Species: *Acholeplasma laidlawii*
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 22-Oct-1999

C:Accession: S33519

R:Boyer, M.J.; Jarhede, T.K.; Tegman, V.; Wieslander, A.
submitted to the EMBL Data Library, June 1993

A:Description: Sequence regions from *Acholeplasma laidlawii* which restore export of beta

A:Reference number: S33518

A:Accession: S33519

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-11 <BOY>

A:Cross-references: EMBL:Z22875; NID:9311706; PIDN:CAM80495.1; PID:9311708

Query Match 29.6%; Score 16; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 7.4e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KQIKHV 8
||:
Db 3 KLVMTTV 10

RESULT 10

S59625
beta-galactosidase alpha chain - *Escherichia coli* (fragment)

C:Species: *Escherichia coli*

C:Date: 20-Jul-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C:Accession: S59625

R:Calugaru, S.V.; Hall, B.G.; Sinnott, M.L.

Biochem. J. 312, 281-286, 1995

A:Title: Catalysis by the large subunit of the second beta-galactosidase of *Escherichia*

A:Reference number: S59625; MUID:96077156; PMID:7492325

A:Accession: S59625

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <CAL>

Query Match 27.8%; Score 15; DB 2; Length 10;
Best Local Similarity 40.0%; Pred. No. 1e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 QKIKH 6
||:
Db 5 ENIQH 9

RESULT 11

S65385

cytochrome-c oxidase (EC 1.9.3.1) chain VIIa, hepatic - rat (fragment)

C:Species: *Rattus norvegicus* (Norway rat)

C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 07-May-1999

C:Accession: S65385

R:Schaeffer, H.; Noack, H.; Halang, W.; Brandt, U.; von Jagow, G.

Eur. J. Biochem. 230, 235-241, 1995

A:Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-term

A:Reference number: S65372; MUID:95324529; PMID:7601105

A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <SCH>
C:Keywords: oxidoreductase

Query Match 27.8%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQK 3
||:
Db 8 KQK 10

RESULT 12

JH0784
neuropeptide TE-6 - pig roundworm (fragment)

C:Species: *Ascaris suum* (pig roundworm)

C:Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 28-Apr-1995

C:Accession: JH0784

R:Smart, D.; Shaw, C.; Curry, W.J.; Johnston, C.F.; Thim, L.; Halton, D.W.; Buchanan,

Biochem. Biophys. Res. Commun. 187, 1323-1329, 1992

A:Title: The primary structure of TE-6: a novel neuropeptide from the nematode *Ascaris*

A:Reference number: JH0784; MUID:93038603; PMID:1417808

A:Accession: JH0784

A:Molecule type: protein

A:Residues: 1-6 <SMA>

A:Experimental source: gonoduct

C:Keywords: neuropeptide

Query Match 25.9%; Score 14; DB 2; Length 6;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KQIK 5
||:
Db 2 KOELE 6

RESULT 13

S78764
ribosomal protein MRP-S23, mitochondrial - bovine (fragment)

C:Species: *Bos primigenius taurus* (cattle)

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: S78764

R:Grack, H.R.

submitted to the Protein Sequence Database, July 1999

A:Reference number: S78760

A:Accession: S78764

A:Molecule type: protein

A:Residues: 1-6 <GRA>

C:Keywords: mitochondrion

F:1-6/Product: ribosomal protein MRP-S23 (fragment) #status experimental <MAT>

Query Match 25.9%; Score 14; DB 2; Length 6;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 HVK 9
||:
Db 2 HVDK 5

RESULT 14

JN0859

peptidyl-dipeptidase A inhibitory peptide C105 - striped bonito

C:Species: *Sarda orientalis* (striped bonito)

C:Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 07-May-1999

C:Accession: JN0859

R:Macsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.

Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993

A:Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory

A:Reference number: JN0859; MUID:94080036; PMID:7764272

A:Accession: JN0859
A:Molecule type: Protein
A:Residues: 1-7 <MAT>
A:Experimental source: Intestine
C:Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin
C:Superfamily: bradykinin-potentiating peptide
C:Keywords: angiotensin-converting enzyme inhibitor

Query Match 25.9% Score 14; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 7 VVKLK 11
| | |
Db 2 VAKLE 6

RESULT 15

A60356
118K stomach cancer antigen - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 17-Mar-1999
C:Accession: A60356
R:Shiraiishi, Y.
Int. J. Cancer 45, 783-787, 1990
A:Title: Western blotting analysis for malignant lymphoma and stomach cancer antigens fr
A:Reference number: A60356; MUID:90216080; PMID:2323853
A:Accession: A60356
A:Molecule type: Protein
A:Residues: 1-9 <SHI>
C:Keywords: glycoprotein

Query Match 25.9% Score 14; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 4 IKHVVKL 10
| | | |
Db 3 LKPVIGL 9

Search completed: February 8, 2003, 10:59:06
Job time : 15 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:58:52 ; Search time 11 Seconds
(without alignments)
22.169 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KQKIKHVYK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 25239

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : Published Applications AA:
1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep.*
12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep.*
13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	51.9	9	10	US-09-984-056-92
2	24	44.4	8	10	US-09-984-056-69
3	24	44.4	8	10	US-09-984-057-69
4	24	44.4	9	10	US-09-834-765-258
5	24	44.4	9	10	US-09-834-765-325
6	24	44.4	9	10	US-09-834-765-643
7	24	44.4	9	10	US-09-872-832-38
8	24	44.4	9	10	US-09-872-832-41
9	24	44.4	10	10	US-09-834-765-89
10	24	44.4	10	10	US-09-834-765-284
11	24	44.4	10	10	US-09-834-765-386
12	24	44.4	10	10	US-09-834-765-666
13	24	44.4	11	10	US-09-734-520-88
14	24	44.4	11	10	US-09-734-520-88
15	24	44.4	11	10	US-10-012-034A-72
16	24	44.4	11	12	US-10-012-034A-88
17	23	40.7	6	9	US-10-105-930-46
18	22	42.6	9	9	US-09-878-603-20
19	22	40.7	10	10	US-09-124-280A-16

20	22	40.7	10	10	US-09-734-520-98	Sequence 98, Appl
21	22	40.7	10	10	US-09-734-520-99	Sequence 99, Appl
22	22	40.7	10	10	US-09-734-520-113	Sequence 113, Appl
23	22	40.7	10	10	US-09-984-056-3	Sequence 3, Appl1
24	22	40.7	10	10	US-09-984-057-3	Sequence 3, Appl1
25	22	40.7	10	12	US-10-012-034A-98	Sequence 98, Appl
26	22	40.7	10	12	US-10-012-034A-99	Sequence 99, Appl
27	22	40.7	11	10	US-09-734-520-57	Sequence 57, Appl
28	22	40.7	11	10	US-09-734-520-102	Sequence 102, Appl
29	22	40.7	11	10	US-09-734-520-104	Sequence 104, Appl
30	22	40.7	11	10	US-09-734-520-109	Sequence 109, Appl
31	22	40.7	11	10	US-09-734-520-111	Sequence 111, Appl
32	22	40.7	11	10	US-09-734-520-112	Sequence 112, Appl
33	22	40.7	11	12	US-10-012-034A-57	Sequence 57, Appl
34	22	40.7	11	12	US-10-012-034A-102	Sequence 102, Appl
35	22	40.7	11	12	US-10-012-034A-104	Sequence 104, Appl
36	22	40.7	11	12	US-10-012-034A-109	Sequence 109, Appl
37	22	40.7	11	12	US-10-012-034A-111	Sequence 111, Appl
38	22	40.7	11	12	US-10-012-034A-112	Sequence 112, Appl
39	22	40.7	11	12	US-10-012-034A-123	Sequence 123, Appl
40	22	40.7	8	9	US-09-933-999A-20	Sequence 20, Appl
41	21	38.9	8	10	US-09-942-121-7	Sequence 7, Appl1
42	21	38.9	9	9	US-09-878-603-23	Sequence 23, Appl
43	21	38.9	9	9	US-09-805-301-3	Sequence 3, Appl1
44	21	38.9	9	10	US-09-826-177-32	Sequence 32, Appl
45	21	38.9	9	10		

ALIGNMENTS

RESULT 1
US-09-984-056-92
Sequence 92, Application US/09984056
Patent No. US20020120106A1
GENERAL INFORMATION:
APPLICANT: BOGOCCH, ELENORE S.
TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
FILE REFERENCE: 09425-46903
CURRENT APPLICATION NUMBER: US/09/984,056
CURRENT FILING DATE: 2001-10-26
PRIOR APPLICATION NUMBER: 60/303,396
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/278,761
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 09/146,755
PRIOR FILING DATE: 1998-09-04
PRIOR APPLICATION NUMBER: 09/817,144
PRIOR FILING DATE: 2001-03-27
PRIOR APPLICATION NUMBER: 08/198,139
PRIOR FILING DATE: 1994-02-17
NUMBER OF SEQ ID NOS: 103
SOFTWARE: PatentIn 2.1
SEQ ID NO 92
LENGTH: 9
TYPE: PRT
ORGANISM: Bacillus anthracis
US-09-984-056-92
Query Match
Best Local Similarity 51.9%; Score 28; DB 10; Length 9;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 5 KHVYK 11
|||:::
Db 1 KHVYK 7
RESULT 2
US-09-984-056-69
Sequence 69, Application US/09984056
Patent No. US20020120106A1

```

: GENERAL INFORMATION:
: APPLICANT: BOGOCCH, ELENORE S.
: TITLE OF INVENTION: ANTHRAX AND SMALL POX REPLICINS AND METHODS OF USE
: FILE REFERENCE: 09425-46903
: CURRENT APPLICATION NUMBER: US/09/984,056
: PRIOR FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: 60/303,396
: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: 60/278,761
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 09/146,755
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: 09/817,144
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 08/198,139
: PRIOR FILING DATE: 1994-02-17
: NUMBER OF SEQ ID NOS: 103
: SOFTWARE: PatentIn 2.1
: SEQ ID NO 69
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-984-056-69
```

```
Query Match          44.4%; Score 24; DB 10; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 3 KIKHVK 9
    | | | | |
Db 1 KKKHTVK 7
```

```

RESULT 3
US-09-984-057-69
: Sequence 69, Application US/09984057
: Patent No. US20020151677A1
: GENERAL INFORMATION:
: APPLICANT: BOGOCCH, SAMUEL
: TITLE OF INVENTION: REPLICINS AND METHODS OF IDENTIFYING
: FILE REFERENCE: 09425-46902
: CURRENT APPLICATION NUMBER: US/09/984,057
: PRIOR FILING DATE: 2001-10-26
: PRIOR APPLICATION NUMBER: 60/303,396
: PRIOR FILING DATE: 2001-07-09
: PRIOR APPLICATION NUMBER: 60/278,761
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 09/146,755
: PRIOR FILING DATE: 1998-09-04
: PRIOR APPLICATION NUMBER: 09/817,144
: PRIOR FILING DATE: 2001-03-27
: PRIOR APPLICATION NUMBER: 08/198,139
: PRIOR FILING DATE: 1994-02-17
: NUMBER OF SEQ ID NOS: 90
: SOFTWARE: PatentIn 2.1
: SEQ ID NO 69
: LENGTH: 8
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-984-057-69
```

```
Query Match          44.4%; Score 24; DB 10; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.1e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 3 KIKHVK 9
    | | | | |
Db 1 KKKHTVK 7
```

```

RESULT 4
US-09-834-765-258
: Sequence 258, Application US/09834765
: Patent No. US20020053478A1
: GENERAL INFORMATION:
: APPLICANT: Mary Paris
: APPLICANT: Pia M. Challita-Eid
: APPLICANT: Arthur B. Raitano
: APPLICANT: Steve Chappell Mitchell
: APPLICANT: Daniel E.H. Afar
: APPLICANT: Aya Jakobovits
: TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
: FILE REFERENCE: 129,6US01
: CURRENT APPLICATION NUMBER: US/09/834,765
: PRIOR FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: 60/197,647
: PRIOR FILING DATE: 2000-04-12
: NUMBER OF SEQ ID NOS: 770
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 258
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-834-765-258
```

```
Query Match          44.4%; Score 24; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 QIKHVK 9
    | : | : |
Db 2 QPYEHVK 9
```

```

RESULT 5
US-09-834-765-325
: Sequence 325, Application US/09834765
: Patent No. US20020055478A1
: GENERAL INFORMATION:
: APPLICANT: Mary Paris
: APPLICANT: Pia M. Challita-Eid
: APPLICANT: Arthur B. Raitano
: APPLICANT: Steve Chappell Mitchell
: APPLICANT: Daniel E.H. Afar
: APPLICANT: Aya Jakobovits
: TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
: FILE REFERENCE: 129,6US01
: CURRENT APPLICATION NUMBER: US/09/834,765
: PRIOR FILING DATE: 2001-09-21
: PRIOR APPLICATION NUMBER: 60/197,647
: PRIOR FILING DATE: 2000-04-12
: NUMBER OF SEQ ID NOS: 770
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 325
: LENGTH: 9
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-834-765-325
```

```
Query Match          44.4%; Score 24; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
OY 2 QIKHVK 9
    | : | : |
Db 2 QPYEHVK 9
```

```

RESULT 6
US-09-834-765-643
: Sequence 643, Application US/09834765
```

```
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.60SU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; PRIOR FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 643
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-643

Query Match          44.4%; Score 24; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 OKIKHVVK 9
        | :||:|
DB      1 QPEYHVVK 8

RESULT 7
US-09-872-832-38
; Sequence 38, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 38
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-832-38

Query Match          44.4%; Score 24; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 OKIKHVVK 9
        | :||:|
DB      1 RRIKEIVK 8

RESULT 8
US-09-872-832-41
; Sequence 41, Application US/09872832
; Patent No. US20020131960A1
; GENERAL INFORMATION:
; APPLICANT: Memorial Sloan-Kettering Cancer Center
; TITLE OF INVENTION: ARTIFICIAL ANTIGEN PRESENTING CELLS AND METHODS OF USE THEREOF
; FILE REFERENCE: 830002-2003.1
; CURRENT APPLICATION NUMBER: US/09/872,832
; CURRENT FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: 60/209,157
; PRIOR FILING DATE: 2000-02-06
```

```
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 41
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-872-832-41

Query Match          44.4%; Score 24; DB 10; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 OKIKHVVK 9
        | :||:|
DB      1 RRVKEIVK 8

RESULT 9
US-09-834-765-89
; Sequence 89, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.60SU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 89
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-89

Query Match          44.4%; Score 24; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 OKIKHVVK 9
        | :||:|
DB      3 QPEYHVVK 10

RESULT 10
US-09-834-765-284
; Sequence 284, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Faris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel E.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; FILE REFERENCE: 129.60SU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 284
```

LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-834-765-284

Query Match 44.4%; Score 24; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 OKIKHVK 9
I :||:|
DB 3 QPEYHVK 10

RESULT 11
US-09-834-765-386
Sequence 386, Application US/09834765
Patent No. US20020055478A1
GENERAL INFORMATION:
APPLICANT: Mary Faris
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
FILE REFERENCE: 129,6USU1
CURRENT APPLICATION NUMBER: US/09/834,765
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/197,647
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 386
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-09-834-765-386

Query Match 44.4%; Score 24; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 OKIKHVK 9
I :||:|
DB 3 QPEYHVK 10

RESULT 12
US-09-834-765-666
Sequence 666, Application US/09834765
Patent No. US20020055478A1
GENERAL INFORMATION:
APPLICANT: Mary Faris
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Arthur B. Raitano
APPLICANT: Steve Chappell Mitchell
APPLICANT: Daniel E.H. Afar
APPLICANT: Aya Jakobovits
TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
FILE REFERENCE: 129,6USU1
CURRENT APPLICATION NUMBER: US/09/834,765
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/197,647
NUMBER OF SEQ ID NOS: 770
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 666
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens

US-09-834-765-666

Query Match 44.4%; Score 24; DB 10; Length 10;
Best Local Similarity 50.0%; Pred. No. 96;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 OKIKHVK 9
I :||:|
DB 1 QPEYHVK 8

RESULT 13
US-09-734-520-72
Sequence 72, Application US/09734520
Patent No. US20020115173A1
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel
TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF
TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE
FILE REFERENCE: 1242,2003-000
CURRENT APPLICATION NUMBER: US/09/734,520
PRIOR FILING DATE: 2000-12-11
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 72
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Fak
NAME/KEY: MYRISTATE
LOCATION: (1)...(0)
NAME/KEY: AMIDATION
LOCATION: (0)...(11)
US-09-734-520-72

Query Match 44.4%; Score 24; DB 10; Length 11;
Best Local Similarity 80.0%; Pred. No. 1,1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HVVKL 10
I :|||
DB 7 HIVKL 11

RESULT 14
US-09-734-520-88
Sequence 88, Application US/09734520
Patent No. US20020115173A1
GENERAL INFORMATION:
APPLICANT: Ben-Sasson, Shmuel
TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF
TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE
FILE REFERENCE: 1242,2003-000
CURRENT APPLICATION NUMBER: US/09/734,520
PRIOR FILING DATE: 2000-12-11
NUMBER OF SEQ ID NOS: 122
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 88
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Ret
NAME/KEY: MYRISTATE
LOCATION: (1)...(0)
NAME/KEY: AMIDATION
LOCATION: (0)...(11)
US-09-734-520-88

Query Match 44.4%; Score 24; DB 10; Length 11;

Best Local Similarity 80.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HVKL 10
11:11
Db 7 HVKL 11

RESULT 15
US-10-012-034A-72

; Sequence 72; Application US/10012034A
; Patent No. US20020137141A1

; GENERAL INFORMATION:

; APPLICANT: Ben-Sasson, Shmuel

; TITLE OF INVENTION: SHORT PEPTIDES FROM THE A-REGION OF

; TITLE OF INVENTION: PROTEIN KINASES WHICH SELECTIVELY MODULATE PROTEIN KINASE

; TITLE OF INVENTION: ACTIVITY

; FILE REFERENCE: BEN-SASSON-5A

; CURRENT APPLICATION NUMBER: US/10/012,034A

; CURRENT FILING DATE: 2001-12-11

; PRIOR APPLICATION NUMBER: 09/734,520

; PRIOR FILING DATE: 2000-12-11

; NUMBER OF SEQ ID NOS: 133

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 72

; LENGTH: 11

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: Fak

; FEATURE:

; NAME/KEY: MYRISTATE

; LOCATION: (1)...(0)

; FEATURE:

; NAME/KEY: AMIDATION

; LOCATION: (0)...(11)

US-10-012-034A-72

Query Match

Best Local Similarity 80.0%; Score 24; DB 12; Length 11;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HVKL 10
11:11
Db 7 HVKL 11

Search completed: February 8, 2003, 11:02:27
Job time : 11 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:54:26 ; Search time 11 Seconds
(without alignments)
41.476 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KOKIKHYVKLK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen parameters: 411

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	18	33.3	10	1	LCMS_LEUMA
2	17	31.5	10	1	COXK_ONCMY
3	15	27.8	9	1	ULAD_HUMAN
4	15	27.8	10	1	AH3_ERUSE
5	15	27.8	10	1	XVNB_DICB4
6	14	25.9	10	1	FARP_LOCM1
7	14	25.9	10	1	NEMS_DROME
8	14	25.9	11	1	CSIS_BACSU
9	14	25.9	11	1	O2OA_COMTE
10	13	24.1	7	1	FAR2_ASCSU
11	13	24.1	9	1	RS10_SERMA
12	13	24.1	10	1	FARP_MANSE
13	13	24.1	10	1	SVK_CAMUP
14	13	24.1	10	1	TKNB_ONCMY
15	13	24.1	10	1	UXA6_CHLTR
16	12	22.2	7	1	HY7_PIG
17	12	22.2	8	1	LPMS_STAEP
18	12	22.2	9	1	MOSH_CLYJA
19	12	22.2	11	1	CXLI_CONMR
20	12	22.2	11	1	UP05_MOUSE
21	12	22.2	11	1	UN05_CLOPA
22	11	20.4	8	1	ACL_THUAL
23	11	20.4	10	1	GRP_RANR1
24	11	20.4	10	1	SPI_HALRO
25	11	20.4	10	1	TKL4_LOCM1
26	10	18.5	7	1	BPP7_BORIN
27	10	18.5	7	1	WMA2_ACHFV
28	10	18.5	8	1	B44K_PORGI
29	10	18.5	8	1	FUSS_FUSSO
30	10	18.5	9	1	NEUX_HUMAN
31	10	18.5	9	1	ULAK_MOUSE
32	10	18.5	9	1	XYLA_STRSO
33	10	18.5	10	1	COXM_RAT

34	10	18.5	11	1	BPP7_AGRHA
35	10	18.5	11	1	MHBI_KLEPN
36	10	18.5	11	1	TIN4_HOPTI
37	9	16.7	3	1	LUXE_VIBPI
38	9	16.7	3	1	THYL_PIG
39	9	16.7	8	1	GLUR_HUMAN
40	9	16.7	9	1	BOK_CLOPA
41	9	16.7	9	1	CONO_CONGE
42	9	16.7	9	1	COXE_THUOB
43	9	16.7	9	1	LITO_LITAU
44	9	16.7	9	1	NSK1_SARBU
45	9	16.7	9	1	PELR_DIAAB

ALIGNMENTS

RESULT 1
LCMS_LEUMA STANDARD: PRT; 10 AA.
AC P21144; P1497;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Leucomyosuppressin (LMS) (Lew-MS).
OS Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
OC Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
CC Blaberidae; Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RM [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE-Head;
RA Holman G.M., Cook B.J., Nachman R.J.;
RT "Isolation, primary structure and synthesis of leucomyosuppressin, an insect neuropeptide that inhibits spontaneous contractions of the cockroach hindgut."
RL Comp. Biochem. Physiol. 85C:329-333(1986).
CC -I- FUNCTION: INHIBITS THE SPONTANEOUS CONTRACTIONS OF COCKROACH PROTODERM (HINDGUT).
KW Neuropeptide; Amidation.
FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SO SEQUENCE 10 AA; 1275 MW; D3C45229D2C1EAB2 CRC64;
Query Match 33.3%; Score 18; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Db 2 OKIKHV 7
1 : 11
1 QVDVHV 6
RESULT 2
COXK_ONCMY STANDARD: PRT; 10 AA.
AC P80332;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cytochrome c oxidase polypeptide V1a-heart (EC 1.9.3.1) (Fragment).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Proteocephale; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;
RM [1]
RP SEQUENCE.
RC TISSUE=Heart;
RX MEDLINE=94237150; PubMed=8181469;
RA Freund R., Kadenbach B.;
RT "Identification of tissue-specific isoforms for subunits Vb and V1a

RT of cytochrome c oxidase isolated from rainbow trout.";
 RL Eur. J. Biochem. 221:1111-1116(1994).
 CC -1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
 CC CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
 CC MITOCHONDRIAL ELECTRON TRANSPORT.
 CC -1- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -1- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VIA FAMILY.
 DR PIR: S43631; S43631.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 10
 SO SEQUENCE 10 AA: 1174 MW: 4C8D81CAFAF772C3 CRC64;
 Query Match 31.5%; Score 17; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

RESULT 3
 ULAD_HUMAN STANDARD: PRT; 9 AA.
 ID ULAD_HUMAN P31929;
 AC P31929;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 106) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8313870;
 RA Hughes G.J., Frutiger S., Paquet N., Pasquali C., Sanchez J.-C.,
 RA Tilsot J.-D., Balroch A., Appel R.D., Hochstrasser D.F.;
 RT "Human liver protein map: update 1993."
 RL Electrophoresis 14:1216-1222(1993).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6, ITS MW IS: 15 kDa.
 DR SWISS-2DPAGE: P31929; HUMAN.
 FT NON_TER 9
 SO SEQUENCE 9 AA: 1129 MW: D02DFB41B6D33322 CRC64;

Query Match 27.8%; Score 15; DB 1; Length 9;
 Best Local Similarity 28.6%; Pred. No. 1.1e+05;
 Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 4
 AH3_PRUSE STANDARD: PRT; 10 AA.
 ID AH3_PRUSE P29261;
 AC P29261;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Amygdalin beta-glucosidase II (EC 3.2.1.117) (Amygdalin hydrolase
 DE Isozyme II) (AH II) (Fragment).
 OS Prunus serotina (Black cherry).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 CC eusteds I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 NCBI_TaxID=23207;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Seed;
 RA Li C.P., Swain E., Poultou J.E.;
 RT "Prunus serotina amygdalin hydrolase and prunasin hydrolase.";
 RL Plant Physiol. 100:282-290(1992).
 CC -1- CATALYTIC ACTIVITY: (R)-amygdalin + H(2)O = (R)-prunasin + D-
 CC glucose.
 CC -1- SUBUNIT: MONOMER.
 CC -1- DEVELOPMENTAL STAGE: ABSENT FROM MATURING BLACK CHERRY FRUITS
 CC UNTIL 6 WEEKS AFTER FLOWERING. THEN, CONCOMITANT WITH COTYLEDON
 CC DEVELOPMENT, THE LEVEL OF ENZYME INCREASES WITH SPECIFICITY FOR
 CC EMBRYONAL TISSUES.
 CC -1- PTM: GLYCOSYLATED.
 KW Glycosidase; Hydrolase; Glycoprotein; Multigene family.
 FT NON_TER 10
 SO SEQUENCE 10 AA: 1033 MW: 3331B8D051E04777 CRC64;

Query Match 27.8%; Score 15; DB 1; Length 10;
 Best Local Similarity 40.0%; Pred. No. 4.1e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 5
 XYNB_DICB4 STANDARD: PRT; 10 AA.
 ID XYNB_DICB4 P80717;
 AC P80717;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Endo-1,4-beta-xylanase B (EC 3.2.1.8) (Xylanase B)
 DE (1,4-beta-D-xylan xylanohydrolase B) (Fragment).
 OS Dictyoglomus sp. (strain B4A).
 CC Bacteria; Dictyoglomus group; Dictyoglomus.
 NCBI_TaxID=69007;
 RN [1]
 RP SEQUENCE.
 RA Adensen A.K., Jacobsen S., Ahling B.K.;
 RL Submitted (OCT-1996) to the SWISS-PROT data bank.
 CC -1- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-xylosidic
 CC linkages in xylans.
 CC -1- PATHWAY: Xylan degradation.
 CC -1- SIMILARITY: BELONGS TO CELLULASE FAMILY F (FAMILY 10 OF GLYCOSYL
 CC HYDROLASES).
 DR InterPro: IPR001000; Glyco_hydro.10.
 DR PROSITE: PS00591; GLYCOSYL_HYDROL_F10; PARTIAL.
 KW xylan degradation; Hydrolase; Glycosidase.
 FT NON_TER 10
 SO SEQUENCE 10 AA: 1144 MW: 4554322AA72041A3 CRC64;

Query Match 27.8%; Score 15; DB 1; Length 10;
 Best Local Similarity 42.9%; Pred. No. 4.1e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 6
 FARP_LOCMI STANDARD: PRT; 10 AA.
 ID FARP_LOCMI P38553;
 AC P38553;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Schistocerca gregaria (PDBVHPLRF-amide) (Cardioexcitatory neuropeptide).
 OS Locusta migratoria (migratory locust), and
 OS Schistocerca gregaria (Desert locust).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;

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OC Insecta; Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
OX Acridoidea; Acrididae; Acrididae; Oedipodinae; Locusta.
RN NCB1_TaxID=7004, 7010;
RP SEQUENCE.
RC SPECIES=L.migratoria; TISSUE=Brain;
RX MEDLINE=9332430; PubMed=7687352;
RA Schoofs L., Holman G.M., Paemen L., Veelaert D., Amelincx M.,
de Loof A.;
RT "Isolation, identification, and synthesis of pDvDFRamide
(SchistofRamide) in Locusta migratoria and its association with the
male accessory glands, the salivary glands, the heart, and the
oviduct.";
RN Peptides 14:409-421(1993).
RN [2]
RP SEQUENCE.
RC SPECIES=S.gregaria; TISSUE=Thoracic nervous system;
RX MEDLINE=8924543; PubMed=2719702;
RA Robb S., Packman L.C., Evans P.D.;
RT "Isolation, primary structure and bioactivity of schistofiramide, a
FMRF-amide-like neuropeptide from the locust, Schistocerca
gregaria.";
RN Biochem. Biophys. Res. Commun. 160:850-856(1989).
CC -I- FUNCTION: MUSCLE INHIBITING AGENT. INVOLVED IN THE NEURAL CONTROL
OF THE VISCERAL MUSCLES OF THE HEART, ACCESSORY GLANDS AND
OVIDUCT. MAY BE INVOLVED IN THE REGULATION OF SALIVA SECRETION.
CC -I- TISSUE SPECIFICITY: FOUND IN AXONS OF THE MALE ACCESSORY GLANDS,
THE SALIVARY GLANDS, THE HEART, AND THE OVIDUCT.
CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
FAMILY.
DR PIR: A32543;
RW Neuropeptide; Amidation.
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1244 MW; D3C51729D2C1EAB2 CRC64;

Query Match 25.9%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 IKHV 7
: 11
DB 3 VDHV 6

RESULT 7
NEMS_DROME STANDARD; PRT: 10 AA.
ID NEMS_DROME
AC P41494:
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Dromyosuppressin (Neomyosuppressin) (NEB-MS).
GN DMS OR NEMS.
OS Drosophila melanogaster (Fruit fly), and
Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
OX NCB1_TaxID=7227, 7385;
RN [1]
RP SEQUENCE.
RC SPECIES=D.melanogaster;
RX MEDLINE=93002195; PubMed=1390001;
RA Nichols R.;
RT "Isolation and structural characterization of Drosophila
TODVDFRamide and FMRFamide-containing neural peptides.";
RN J. Mol. Neurosci. 3:213-218(1992).
RN [2]
RP SEQUENCE.
RC SPECIES=S.bullata; TISSUE=Head;
RX MEDLINE=9304786; PubMed=1358537;
RA Fonagy A., Schoofs L., Proost P., Van Damme J., Bueds H., De Loof A.;
RT "Isolation, primary structure and synthesis of neomyosuppressin, a

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RT myoinhibiting neuropeptide from the grey fleshfly, Neobellieria
bullata.";
RN Comp. Biochem. Physiol. 102C:239-245(1992).
CC -I- FUNCTION: MYOINHIBITING NEUROPEPTIDE.
DR FlyBase; FBgn0011581; Dms.
RW Neuropeptide; Amidation.
FT MOD_RES 10
SQ SEQUENCE 10 AA; 1248 MW; D3C00329D2C1EAB2 CRC64;

Query Match 25.9%; Score 14; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 IKHV 7
: 11
DB 3 VDHV 6

RESULT 8
CS15_BACSU STANDARD; PRT: 11 AA.
ID CS15_BACSU
AC P81095;
DT 15-JUN-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Cold shock protein CS15 (11 kDa cold shock protein) (Fragment).
OS Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCB1_TaxID=1423;
RN [1]
RP SEQUENCE.
RC STRAIN=168 / JH642;
RA Graumann P.L., Schmid R., Marahiel M.A.;
RT Submitted (OCT-1997) to the SWISS-PROT data bank.
RN [2]
RP CHARACTERIZATION
RC STRAIN=168 / JH642;
RX MEDLINE=96345629; PubMed=8755892;
RA Graumann P., Schroeder K., Schmid R., Marahiel M.A.;
RT "Cold shock stress-induced proteins in Bacillus subtilis.";
RN J. Bacteriol. 178:4611-4619(1996).
CC -I- SUBCELLULAR LOCATION: Cytoplasmic.
CC -I- INDUCTION: IN RESPONSE TO LOW TEMPERATURE.
CC -I- CAUTION: Could not be found in the genome of B.subtilis 168.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1360 MW; 15F6CEB6322C330 CRC64;

Query Match 25.9%; Score 14; DB 1; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.8e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 8 VKLK 11
: 11
DB 4 IKVK 7

RESULT 9
Q20A_COMTE STANDARD; PRT: 11 AA.
ID Q20A_COMTE
AC P80464;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Quinolone 2-oxidoreductase, alpha chain (EC 1.3.99.17) (Fragment).
OS Comamonas testosteroni (Pseudomonas testosteroni).
OC Bacteria; Proteobacteria; beta subdivision; Comamonadaceae; Comamonas.
OX NCB1_TaxID=285;
RN [1]
RP SEQUENCE.
RC STRAIN=63;
RX MEDLINE=96035889; PubMed=7556204;
RA Schach S., Tshisuka B., Fetzner S., Lingens F.;
RT "Quinolone 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-

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RT dioxigenase from *Comamonas testosteroni* 63. The first two enzymes in
 RT quinolone and 3-methylquinoline degradation.";
 RL Eur. J. Biochem. 232:536-544(1995).
 CC -1- FUNCTION: CONVERTS (3-METHYL-)-QUINOLINE TO (3-METHYL-)-2-OXO-
 CC 1,2-DIHYDROQUINOLINE.
 CC -1- CATALYTIC ACTIVITY: Quinolone + acceptor + H(2)O = Isoquinolin-
 CC 1(2H)-one + reduced acceptor.
 CC -1- COFACTOR: FAD, MOLYBDENUM AND IRON-SULFUR.
 CC -1- PATHWAY: FIRST STEP IN THE DEGRADATION OF QUINOLINE AND
 CC (3-METHYL-)-QUINOLINE.
 CC -1- SUBUNIT: HETEROHEXAMER OF TWO ALPHA CHAINS, TWO BETA CHAINS, AND
 CC TWO GAMMA CHAINS (PROBABLE).
 KM Oxidoreductase; Flavoprotein; FAD; Molybdenum.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1213 MW: 869094322B1DC2CA CRC64:
 Query Match 25.9%; Score 14; DB 1; Length 11;
 Best Local Similarity 60.0%; Pred. No. 6.8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 7 VKLK 11
 DB 5 VAEK 9
 RESULT 10
 FAR2_ASCSU STANDARD: PRT: 7 AA.
 ID FAR2_ASCSU P31890:
 AC 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFamide-like neuropeptide AF2.
 OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides), and
 OS Panagrellus redivivus.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
 CC Ascarididae; Ascaris.
 CC NCB1_TaxID=6233; 6233;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=A.suum;
 RX MEDLINE=93324431; PubMed=8332542;
 RA Cowden C., Stretton A.O.W.;
 RT "AF2, an Ascaris neuropeptide: Isolation, sequence, and bioactivity.";
 RL Peptides 14:423-430(1993).
 RN [2]
 RP SEQUENCE.
 RC SPECIES=P.redivivus;
 RX MEDLINE=95060998; PubMed=7970891;
 RA Maule A.G., Shaw C., Bowman J.W.;
 RT "The FMRFamide-like neuropeptide AF2 (Ascaris suum) is present in the
 RL free-living nematode, Panagrellus redivivus (Nematoda, Rhabdilitida).";
 RL Parasitology 109:351-356(1994).
 CC -1- FUNCTION: HAS EFFECTS ON MUSCLE TENSION.
 CC -1- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
 CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 KM Neuropeptide; Amidation.
 FT MOD_RES 7
 SQ SEQUENCE 7 AA: 992 MW: 69040735B1E350 CRC64:
 Query Match 24.1%; Score 13; DB 1; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 KH 6
 DB 1 KH 2
 RESULT 11
 RS10_SERMA - - -

ID RS10_SERMA STANDARD: PRT: 9 AA.
 AC 068936:
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 30S ribosomal protein S10 (Fragment).
 GN RPSJ.
 OS Serratia marcescens.
 CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 CC Serratia.
 CC NCB1_TaxID=615;
 RN [1]
 RP SEQUENCE FROM N.A.
 RL Noorani S.M., Lindahl L., Zengel J.M.;
 RT Submitted (APR-1998) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: Involved in the binding of tRNA to the ribosomes (By
 CC similarity).
 CC -1- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; AF058451; AAC14294.1;
 DR InterPro; IPR001848; Ribosomal_S10.
 DR PROSITE; PS00361; RIBOSOMAL_S10; PARTIAL.
 KM Ribosomal protein.
 FT NON_TER 9
 SQ SEQUENCE 9 AA: 1214 MW: DE394400416D456 CRC64:
 Query Match 24.1%; Score 13; DB 1; Length 9;
 Best Local Similarity 50.0%; Pred. No. 1.1e+05;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 2 QIK 5
 DB 4 QIR 7
 RESULT 12
 FARP_MANSE STANDARD: PRT: 10 AA.
 ID FARP_MANSE P18523:
 AC 01-NOV-1990 (Rel. 16, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE FMRFamide-like neuropeptide.
 OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 CC Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
 CC Insecta; Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata;
 CC Dictyria; Sphingioidea; Sphingidae; Sphinginae; Manduca.
 CC NCB1_TaxID=7130;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=91045350; PubMed=2235684;
 RA Kingan T.G., Teplov D.B., Phillips J.M., Rietm J.P., Rao K.R.,
 RA Hildebrand J.G., Homberg U., Kammer A.E., Jardine I., Griffin P.R.,
 RA Hunt D.F.;
 RT "A new peptide in the FMRFamide family isolated from the CNS of the
 RL hawkmoth Manduca sexta.";
 RL Peptides 11:849-856(1990).
 CC -1- FUNCTION: INCREASES THE FORCE OF NEURALLY EVOKED CONTRACTIONS IN
 CC THE MAJOR POWER-PRODUCING FLIGHT MUSCLES, THE DORSAL LONGITUDINAL
 CC MUSCLES AND SO IS LIKELY TO PLAY A ROLE IN SUSTAINING OR PROMOTING
 CC FLIGHT BEHAVIOR PATTERNS.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 CC FAMILY.
 DR PIR; A43977; A43977.
 KM Amidation; Neuropeptide.

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FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA: 1247 MW: D3C45229D5B1F2D2 CRC64;

Query Match
Best Local Similarity 40.0%; Score 13; DB 1; Length 10;
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 OKIKH 6
   1 : 1
Db 1 ODVYH 5

RESULT 13
STR_CAMUP
ID SYK_CAMUP STANDARD: PRT: 10 AA.
AC 046464;
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LysRS)
DE (Fragment).
GN LYS.
OS Campylobacter upsaliensis.
OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC Campylobacter.
OX NCBI_TaxID=28080;
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 43954;
RX MEDLINE=97149302; PubMed=8996110;
RA Bourke B., Rashid S.F., Bingham H.L., Chan V.L.;
RT "Characterization of Campylobacter upsaliensis fur and its
RT localization in a highly conserved region of the Campylobacter
RT genome."
RL Gene 183:219-224(1996).
CC -i- CATALYTIC ACTIVITY: ATP + L-Lysine + tRNA(Lys) -> AMP + diphosphate
CC + L-Lysyl-tRNA(Lys).
CC -i- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -i- SUBCELLULAR LOCATION: Cytoplasmic.
CC -i- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: L7076; ABA41342.1;
DR InterPro: IPR002106; AA:RNA_Ligase.II.
DR PROSITE: PS50862; AA:RNA_Ligase.II; PARTIAL.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT NON_TER 1
SQ SEQUENCE 10 AA: 1218 MW: 9CEA46AB13372B05 CRC64;

Query Match
Best Local Similarity 40.0%; Score 13; DB 1; Length 10;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOKIK 5
   1 : 1
Db 2 KSELK 6

RESULT 14
TKNB_ONCMY
ID TKNB_ONCMY STANDARD: PRT: 10 AA.
AC P28500;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)

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DE Neurokinin A (Substance K) (Neuromedin L).
OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri), and
OS Gadus morhua (Atlantic cod).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022, 8049;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92298992; PubMed=1376687;
RA Jensen J., Conlon J.M.;
RT "Substance-P-related and neurokinin-A-related peptides from the brain
RT of the cod and trout."
RL Eur. J. Biochem. 206:659-664(1992).
CC -i- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -i- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
CC PIR: S23186; S23186.
DR InterPro: IPR002040; Tachykinin.
DR PROSITE: PS00267; TACHYKININ: 1.
KW Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10
SQ SEQUENCE 10 AA: 1145 MW: 136B4062C9D5B440 CRC64;

Query Match
Best Local Similarity 50.0%; Score 13; DB 1; Length 10;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 KIKHVVK 10
   1 : 1
Db 2 KINSFVL 9

RESULT 15
UXA6_CHLTR
ID UXA6_CHLTR STANDARD: PRT: 10 AA.
AC P38007;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Unknown protein from 2D-page from elementary body (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE.
RC STRAIN=L2/434/Bu;
RA Binl L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M.,
RA Comanducci M., Christensen G., Birkelund S., Verecu E., Ratti G.,
RA Pallini V.;
RL Submitted (SEP-1994) to the SWISS-PROT data bank.
CC -i- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 6.44, ITS MW IS: 38.6 kDa.
DR Sienna-2DPAGE: P38007;
FT NON_TER 10
SQ SEQUENCE 10 AA: 1243 MW: DAD39A33304B5339 CRC64;

Query Match
Best Local Similarity 40.0%; Score 13; DB 1; Length 10;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 5 KHVVK 9
   1 : 1
Db 4 KYIKK 8

```

Search completed: February 8, 2003, 10:58:10
Job time : 12 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:56:36 ; Search time 28 Seconds
(without alignments)
80.947 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KQKIKHVVKLK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1588

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriophage:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	20	37.0	7	12	Q66205	Q66205 transmissib
2	20	37.0	8	8	Q34909	Q34909 locusta mig
3	20	37.0	11	2	Q56413	Q56413 escherichia
4	19	35.2	8	2	P83158	P83158 anabaena sp
5	19	35.2	8	3	Q05403	Q05403 saccharomyc
6	19	35.2	9	10	Q9FEC0	Q9FEC0 hordeum vul
7	19	35.2	10	2	Q9JN49	Q9JN49 staphylococ
8	18	33.3	9	6	Q9R9C4	Q9R9C4 borrelia bu
9	18	33.3	10	2	Q9XSL0	Q9XSL0 capra hircu
10	18	33.3	10	2	Q52762	Q52762 rhizobium s
11	18	33.3	10	2	Q8VN85	Q8VN85 helicobacte
12	17	31.5	11	2	Q9S618	Q9S618 prochloroco
13	16	29.6	9	11	Q99MG3	Q99MG3 mus musculi
14	16	29.6	10	4	Q8WXB5	Q8WXB5 homo sapien
15	16	29.6	11	2	Q44090	Q44090 achloleplasm
16	16	29.6	11	8	Q32704	Q32704 nicotiana t

17	16	29.6	11	10	Q8RUE7	Q8RUE7 zea mays (m
18	16	29.6	11	11	Q9QVDA	Q9QVDA ratius sp.
19	16	29.6	11	12	P89269	P89269 xestia c-ni
20	15	27.8	8	2	Q56759	Q56759 xanthobacte
21	15	27.8	11	2	Q9R8V0	Q9R8V0 pseudomonas
22	15	27.8	11	2	Q9LAF7	Q9LAF7 bacillus ce
23	15	27.8	11	4	Q9H4H5	Q9H4H5 homo sapien
24	15	27.8	11	7	Q77880	Q77880 oreochromis
25	15	27.8	11	7	Q77897	Q77897 oreochromis
26	15	27.8	11	7	Q77907	Q77907 oreochromis
27	15	27.8	11	8	Q9GH12	Q9GH12 pandorina m
28	15	27.8	11	11	Q9QXF6	Q9QXF6 mus musculi
29	14	25.9	8	5	Q9N6M5	Q9N6M5 toxoplasma
30	14	25.9	8	6	Q9XSY1	Q9XSY1 canis fami
31	14	25.9	8	8	Q9GD47	Q9GD47 hydrilastele
32	14	25.9	8	8	Q9GC24	Q9GC24 nenga punil
33	14	25.9	8	10	Q42507	Q42507 triticum ae
34	14	25.9	8	11	Q9ET21	Q9ET21 mus musculi
35	14	25.9	8	12	Q84271	Q84271 human papil
36	14	25.9	8	12	Q84273	Q84273 human papil
37	14	25.9	8	12	Q9E806	Q9E806 beet soil-b
38	14	25.9	8	12	Q9E807	Q9E807 beet soil-b
39	14	25.9	8	12	Q9DSN6	Q9DSN6 beet soil-b
40	14	25.9	8	12	Q9E805	Q9E805 beet soil-b
41	14	25.9	8	12	Q9E804	Q9E804 beet soil-b
42	14	25.9	8	12	Q9DSN5	Q9DSN5 beet soil-b
43	14	25.9	8	12	Q9E803	Q9E803 beet soil-b
44	14	25.9	8	12	Q9DSN4	Q9DSN4 beet soil-b
45	14	25.9	8	12	Q9DSN3	Q9DSN3 beet soil-b

ALIGNMENTS

RESULT 1

ID	Q66205	PRELIMINARY:	PRT:	7 AA.
AC	Q66205:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			
DR	01-NOV-1996 (TREMBLrel. 01, Last sequence update)			
DT	01-DEC-2001 (TREMBLrel. 19, Last annotation update)			
DE	Membrane protein (1 is 3rd base in codon) (Fragment).			
OS	Transmissible gastroenteritis virus.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;			
OC	Coronaviridae; Coronavirus.			
OX	NCBI_TaxID=11149;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=F5772/70;			
RA	MEDLINE=88216185; PubMed=2835592;			
RT	Britton P., Carmenes R.S., Page K.W., Garves D.J., Parra F.;			
RT	"Sequence of the Nucleoprotein Gene from a Virulent British Field			
RT	Isolate of Transmissible Gastroenteritis Virus and Its Expression in			
RT	Saccharomyces Cerevisiae."			
RL	MOL. Microbiol. 2:89-99(1988).			
DR	EMBL, Y00542; CAA68606.1; -.			
FT	NON_TER			
SQ	SEQUENCE 7 AA: 869 MW; 72C691E727233B70 CRC64;			
	Query Match	37.0%;	Score 20;	DB 12; Length 7;
	Best Local Similarity	42.9%;	Pred. NO. 6.7e+05;	
	Matches	3; Conservative	3; Mismatches	1; Indels
				Gaps 0;
QY	2 QKIKHV 8			
	: 1: 1:1			
DB	1 EKLHMV 7			
RESULT 2				
ID	Q34909	PRELIMINARY:	PRT:	8 AA.
AC	Q34909:			
DT	01-NOV-1996 (TREMBLrel. 01, Created)			

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Cytochrome b (Fragment).
 OS Locusta migratoria (Migratory locust).
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caellifera;
 OC Acridocephala; Acrididae; Acrididae; Oedipodinae; Locusta.
 OX NCBI_TaxID=7004;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88223478; PubMed=2836084;
 RA McCracken A., Uhlenbusch I., Gellissen G.;
 RT "Structure of the cloned Locusta migratoria mitochondrial genome:
 RT restriction mapping and sequence of its ND-1 (URF-1) gene.";
 RL Curr. Genet. 11:625-630(1987).
 DR EMBL: X05286; CAA28905.1; -.
 KW Mitochondrion.
 FT NON_TER 1
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 1019 MW; F8E33723304B45B6 CRC64;

Query Match 37.0%; Score 20; DB 8; Length 8;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KIKH 6
 1:11
 DB 5 KIKH 8

RESULT 3
 ID 056413 PRELIMINARY; PRT; 11 AA.
 AC 056413:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE IS602L region DNA, 5' end (Fragment).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX TRANSPOSON-TRANSPOSON TN602;
 RX MEDLINE=87318208; PubMed=2819910;
 RA Stibletz S., Davies J.E.;
 RT "Tn602: A naturally occurring relative of Tn903 with direct repeats.";
 RL Plasmid 17:202-209(1987).
 DR EMBL: M22735; AAA27464.1; -.
 FT NON_TER 1
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1361 MW; 447E8354A05339C3 CRC64;

Query Match 37.0%; Score 20; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 4.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQIK 5
 1:11
 DB 2 KQIK 6

RESULT 4
 ID P83158 PRELIMINARY; PRT; 8 AA.
 AC P83158:
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DIC-2001 (TREMBlrel. 19, Last annotation update)
 DE Photosystem I iron-sulfur center (Photosystem I subunit VIII) (9 kDa polypeptide) (PSI-C) (Fragment).

OS Anabaena sp. (strain L31).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
 OX NCBI_TaxID=29412;
 RN [1]
 RP SEQUENCE.
 RA Apte S.K., Uhlemann E., Schmid R., Altendorf K.;
 RL Submitted (OCT-2001) to the SWISS-PROT data bank.
 CC -!- FUNCTION: APOPROTEIN FOR THE IRON-SULFUR CENTERS FA AND FB OF THE PHOTOSYSTEM I COMPLEX.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF 'BACTERIAL-TYPE' 4FE-4S FERREDOXINS.
 DR InterPro: IPR001450; 4FE4S_FERREDOXIN.
 DR PROSITE: PS00198; 4FE4S_FERREDOXIN; PARTIAL.
 KW Photosynthesis; Photosystem I; Iron-sulfur; 4Fe-4S; Metal-binding.
 FT NON_TER 8
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 962 MW; C5B505322D1A1F5 CRC64;

Query Match 35.2%; Score 19; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 HVKL 10
 1:11
 DB 2 HVKL 6

RESULT 5
 ID 005403 PRELIMINARY; PRT; 8 AA.
 AC 005403:
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE DNA for ORF's from chromosome XV (Fragment).
 GN COQ3 AND YOL096C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycos.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=EY1679;
 RX MEDLINE=96021609; PubMed=8533473;
 RA Zumbstein E., Pearson B.M., Kalogeropoulos A., Schwelzer M.;
 RT "A 29.425 kb segment on the left arm of yeast chromosome XV contains more than twice as many unknown as known open reading frames.";
 RL Yeast 11:975-986(1995).
 DR EMBL: X83121; CAA58183.1; -.
 DR SGD: S0005456; COQ3.
 FT NON_TER 8
 FT NON_TER 8
 SQ SEQUENCE 8 AA; 879 MW; 7B5322D2C4A1E058 CRC64;

Query Match 35.2%; Score 19; DB 3; Length 8;
 Best Local Similarity 57.1%; Pred. No. 6.7e+05;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 IKHVKL 10
 1:1111
 DB 2 IKHVKL 8

RESULT 6
 ID 09FEC0 PRELIMINARY; PRT; 9 AA.
 AC 09FEC0:
 DT 01-MAR-2001 (TREMBlrel. 16, Created)
 DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
 DE MaluORF.
 GN MAL.
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;


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OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
OX Triticeae; Hordeum.
RN NCBL_TaxID=4513;
RP SEQUENCE FROM N.A.
RC SRRAIN-CV, ALGERIAN:
RA Zhou F., Kurth J., Wei F., Elliott C., Vale G., Yahiaoui N.,
RA Keller B., Somerville S., Wise R., Schulze-Lefert P.;
RT "Cell-autonomous Expression of Barley Ml1 Confers Race-specific
RT Resistance to the Powdery Mildew Fungus via a Rar1 Independent
RT Signaling Pathway";
RL Plant Cell 0:0-0(2001).
DR EMBL; AY009939; AAC37357.1; -.
DR EMBL; AY009938; AAC37355.1; -.
SQ SEQUENCE 9 AA; 1163 MW; 473E2440573B5337 CRC64;

Query Match
Best Local Similarity 35.2%; Score 19; DB 10; Length 9;
Matches 2; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 IKHVXK 11
Db 2 LKYLINLR 9

RESULT 7
Q9JN49 PRELIMINARY; PRT; 10 AA.
ID Q9JN49;
AC Q9JN49;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE Plasmid PE194 ermC leader region (Fragment).
OC Staphylococcus aureus.
OC Plasmid PE194.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Staphylococcus.
OX NCBL_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86041917; PubMed=3903662;
RA Narayanan C.S., Dubnau D.;
RT "Evidence for the translational attenuation model: ribosome-binding
RT studies and structural analysis with an in vitro run-off transcript
RT of ermC.";
RL Nucleic Acids Res. 13:7307-7326(1985).
KW EMBL; X03097; CAA26883.1; -.
KM Plasmid.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1228 MW; 6B6C88E33054433B CRC64;

Query Match
Best Local Similarity 35.2%; Score 19; DB 2; Length 10;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KQKIKH 6
Db 3 EKNIKH 8

RESULT 8
Q9R9C4 PRELIMINARY; PRT; 9 AA.
ID Q9R9C4;
AC Q9R9C4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE Plasmid cp2-2, possible partition proteins (Fragment).
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid cp2-2.
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBL_TaxID=139;
RN [1]

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RP SEQUENCE FROM N.A.
RC STRAIN-B31;
RX MEDLINE=98361033; PubMed=9695920;
RA Stevenson B., Casjens S., Rosa P.;
RT "Evidence of past recombination events among the genes encoding the
RT Erp antigens of Borrelia burgdorferi.";
RL Microbiology 144:1869-1879(1998).
DR EMBL; AF022479; AAC35438.1; -.
KW Plasmid.
FT NON_TER 1 1
SQ SEQUENCE 9 AA; 1155 MW; 4E1A244330504373 CRC64;

Query Match
Best Local Similarity 33.3%; Score 18; DB 2; Length 9;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 IKHVXK 9
Db 1 IKWLTK 6

RESULT 9
Q9XSLO PRELIMINARY; PRT; 9 AA.
ID Q9XSLO;
AC Q9XSLO;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Alpha s2-casein (Fragment).
CN CSN152.
OS Capra hircus (goat).
OC Eukaryota; Metazoa; Chordata; Cranialia; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBL_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=21313038; PubMed=11419340;
RA Ramunno L., Longobardi E., Pappalardo M., Rando A., Di Gregorio P.,
RA Cosenza G., Mariani P., Pastore N., Masina P.;
RT "An allele associated with a non detectable amount of as2 casein in
RT goat milk.";
RL Anim. Genet. 32:19-26(2001).
DR EMBL; AJ238475; CAB44298.1; -.
FT NON_TER 1 1
FT VARIANT 5 5 I -> V.
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1047 MW; AAA2A5A5B051EB16 CRC64;

Query Match
Best Local Similarity 33.3%; Score 18; DB 6; Length 9;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KIKHV 7
Db 1 KMEHI 5

RESULT 10
Q52762 PRELIMINARY; PRT; 10 AA.
ID Q52762;
AC Q52762;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Dinitrogenase beta subunit (Fragment).
OS Rhizobium sp. cowpea (strain IRc78).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Rhizobiaceae; Rhizobium.
OX NCBL_TaxID=400;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN-IRC78;
RA Yun A.C., Szalay A.A.;
RT "Structural genes of dinitrogenase and dinitrogenase reductase are
transcribed from two separate promoters in the broad host range compa
RT Rhizobium strain IRC78.";
RL Proc. Natl. Acad. Sci. U.S.A. 81:7358-7362(1984).
DR EMBL; M10203; AAA26309.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1100 MW; CFFD0BC1EB1DC5A6 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 8.7e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 OKIKHV 8
Db 3 QSAEHL 9

RESULT 11
Q8VN85 PRELIMINARY; PRT; 10 AA.
AC Q8VN85;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DE Urease accessory protein.
GN URE.
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
OC Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NO267;
RX MEDLINE=21625040; PubMed=11742075;
RA Falush D., Kraft C., Taylor N.S., Correa P., Fox J.G., Achtman M.,
RT "Recombination and mutation during long-term gastric colonization by
RT Helicobacter pylori: Estimates of clock rates, recombination size and
RT minimal age.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:15056-15061(2001).
DR EMBL; A418329; CAD11229.1; -.
SQ SEQUENCE 10 AA; 1329 MW; 81E8020403332411 CRC64;

Query Match 33.3%; Score 18; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 KOKIKH 6
Db 5 KKREKH 10

RESULT 12
Q9S618 PRELIMINARY; PRT; 11 AA.
AC Q9S618;
DT 01-MAY-2000 (TREMblrel. 13, Created)
DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE Cytochrome b6/f complex subunit IV (Fragment).
GN PETD.
OS Prochlorococcus sp.
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;
OC Prochlorococcus.
OX NCBI_TaxID=1220;
RN [1]
RP SEQUENCE FROM N.A.
RA Urbach E., Chisholm S.W.;
RT "Genetic diversity in Prochlorococcus populations flow cytometrically
RT sorted from the Sargasso Sea and Gulf Stream.";
RL Limnol. Oceanogr. 43:1615-1630(1998).

DR EMBL; AF070132; AAD20740.1; -.
FT NON_TER 11
SQ SEQUENCE 11 AA; 1297 MW; 5CC38013B7633337 CRC64;

Query Match 31.5%; Score 17; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.4e+04;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HVVK 9
Db 2 HILK 5

RESULT 13
Q99MG3 PRELIMINARY; PRT; 9 AA.
ID Q99MG3;
AC Q99MG3;
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE NRCAM protein (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA More M.I., Kirsch F.P., Rathjen F.G.;
RT "Targeted ablation of Nrcam and ankyrin-B results in disorganized lens
RT fibres leading to cataract formation.";
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF346472; AAK25814.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1039 MW; 32FCB721E333327 CRC64;

Query Match 29.6%; Score 16; DB 1; Length 9;
Best Local Similarity 60.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KIKHV 7
Db 3 KKKHL 7

RESULT 14
Q8WXB5 PRELIMINARY; PRT; 10 AA.
ID Q8WXB5;
AC Q8WXB5;
DT 01-MAR-2002 (TREMblrel. 20, Created)
DT 01-MAR-2002 (TREMblrel. 20, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE EYA2B (Fragment).
GN EYA2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Fee B.E., Doyle C.A., Cleveland J.L.;
RT "A novel eyes absent protein is expressed in the human eye.";
RL Gene 0:0-0(2002).
DR EMBL; AF455148; AAL57875.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA; 1298 MW; 18021202C69B132B CRC64;

Query Match 29.6%; Score 16; DB 4; Length 10;
Best Local Similarity 37.5%; Pred. No. 2e+04;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KIKHVKL 10
Db 2 RYKEMVEL 9

RESULT 15
044090

PRELIMINARY; PRT: 11 AA.

AC 044090;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Hypothetical export segment (Fragment).
OS Acholeplasma laidlawii;
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Acholeplasmatales; Acholeplasmataceae; Acholeplasma.
OX NCBI_TaxID=2148;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A-EF22;

RA Boyer M.J., Jarhede T.K., Tegman V., Wieslander A.;
RT "Sequence regions from Acholeplasma laidlawii which restore export of
beta-lactamase in Escherichia coli."
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
DR EMBL; Z22875; CAA80495.1; -
FT NON_TER 11
SQ SEQUENCE 11 AA: 1234 MW: 5C9D2AE8A682C337 CRC64;

Query Match 29.6%; Score 16; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.1e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOKIKHV 8
I I I I
Db 3 KUKVMTVV 10

Search completed: February 8, 2003, 10:58:45
Job time : 29 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2003, 10:57:57 ; Search time 132 Seconds
(Without alignments)
53.728 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 KOKIKHVKLK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 450623

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pending_Patents_AA_Main: *
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2: /cgn2_6/ptodata/1/paa/US06_COMB.pep: *
3: /cgn2_6/ptodata/1/paa/US07_COMB.pep: *
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9: /cgn2_6/ptodata/1/paa/US085_COMB.pep: *
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27: /cgn2_6/ptodata/1/paa/US60_COMB.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	54	100.0	11	7	US-08-318-892-3
2	54	100.0	11	7	US-08-318-892B-3
3	54	100.0	11	15	US-09-169-077-1
4	54	100.0	11	18	US-09-424-292-4
5	54	100.0	11	20	US-09-685-010-30
6	54	100.0	11	23	US-09-978-309A-30

7	49	90.7	10	18	US-09-424-292-7	Sequence 7, Appl1
8	45	83.3	9	7	US-08-318-892B-30	Sequence 30, Appl1
9	45	83.3	9	20	US-09-685-010-60	Sequence 60, Appl1
10	45	83.3	9	23	US-09-978-309A-60	Sequence 60, Appl1
11	44	81.5	9	7	US-08-318-892B-31	Sequence 31, Appl1
12	41	75.9	10	18	US-09-424-292-8	Sequence 8, Appl1
13	34	63.0	7	18	US-09-424-292-11	Sequence 11, Appl1
14	31	57.4	9	8	US-08-474-654-29	Sequence 29, Appl1
15	31	57.4	9	8	US-08-474-654-39	Sequence 39, Appl1
16	31	57.4	9	14	US-09-052-530-263	Sequence 263, Appl
17	31	57.4	9	18	US-09-412-863-4056	Sequence 4056, Ap
18	31	57.4	9	18	US-09-412-863-12607	Sequence 12607, A
19	31	57.4	9	27	US-60-272-565-76	Sequence 76, Appl
20	31	57.4	9	18	US-09-412-863-5662	Sequence 5662, Ap
21	29	53.7	9	8	US-08-474-654-25	Sequence 25, Appl
22	29	53.7	9	8	US-08-474-654-34	Sequence 34, Appl
23	28	51.9	9	1	PCT-US02-21494-92	Sequence 92, Appl
24	28	51.9	9	8	US-08-474-654-27	Sequence 27, Appl
25	28	51.9	9	8	US-08-474-654-28	Sequence 28, Appl
26	28	51.9	9	8	US-08-474-654-37	Sequence 37, Appl
27	28	51.9	9	8	US-08-474-654-38	Sequence 38, Appl
28	28	51.9	9	23	US-09-984-056-92	Sequence 92, Appl
29	28	51.9	9	25	US-10-105-232-92	Sequence 92, Appl
30	28	51.9	9	27	US-60-272-565-87	Sequence 87, Appl
31	27	50.0	8	18	US-09-412-863-1020	Sequence 1020, Ap
32	27	50.0	8	18	US-09-412-863-5611	Sequence 5611, Ap
33	27	50.0	8	18	US-09-412-863-5613	Sequence 5613, Ap
34	27	50.0	8	18	US-09-412-863-8962	Sequence 8962, Ap
35	27	50.0	9	18	US-09-412-863-13736	Sequence 13736, A
36	27	50.0	10	18	US-09-412-863-2991	Sequence 2991, Ap
37	27	50.0	10	18	US-09-412-863-8970	Sequence 8970, Ap
38	27	50.0	10	18	US-09-412-863-11204	Sequence 11204, A
39	27	50.0	10	25	US-10-109-274A-11	Sequence 11, Appl
40	26	48.1	7	18	US-09-424-292-13	Sequence 13, Appl
41	26	48.1	7	19	US-09-500-904A-72	Sequence 72, Appl
42	26	48.1	9	8	US-08-474-654-33	Sequence 33, Appl
43	26	48.1	9	8	US-08-474-654-24	Sequence 24, Appl
44	26	48.1	9	8	US-08-474-654-32	Sequence 32, Appl
45	26	48.1	9	8	US-08-474-654-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-08-318-892-3
: Sequence 3, Application US/08318892
: GENERAL INFORMATION:
: APPLICANT: Tuttle, Eva A
: TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR
: TITLE OF INVENTION: FOR HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING
: TITLE OF INVENTION: PEPTIDES
: NUMBER OF SEQUENCES: 29
: CORRESPONDENCE ADDRESS:
: ADDRESS: C/O FISH & NEAVE
: STREET: 1251 Avenue of the Americas
: CITY: New York
: STATE: N.Y.
: COUNTRY: USA
: ZIP: 10020
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Wordperfect 6.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/318,892
: FILING DATE: 1-DEC-1994
: CLASSIFICATION: 536
: ATTORNEY/AGENT INFORMATION:
: NAME: Pierri, Margaret A
: REGISTRATION NUMBER: 30,709
: REFERENCE/DOCKET NUMBER: SIM-8

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-892-3

Query Match          100.0%; Score 54; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOKIKHVYK 11
DB 1 KOKIKHVYK 11

RESULT 2
US-08-318-892B-3
; Sequence 3, Application US/08318892B
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR FOR
; TITLE OF INVENTION: HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING PEPTIDES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,892B
; FILING DATE: 1-DEC-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pierri, Margaret A
; REGISTRATION NUMBER: 30709
; REFERENCE/DOCKET NUMBER: SIM-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-892B-3

Query Match          100.0%; Score 54; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOKIKHVYK 11
DB 1 KOKIKHVYK 11

RESULT 3
US-09-169-077-1
; Sequence 1, Application US/09169077
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; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN HYALURONAN RECEPTOR
; NUMBER OF SEQUENCES: 52
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,077
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CA97/00240
; FILING DATE:
; APPLICATION NUMBER: GB 9607441.4
; FILING DATE: 10-APR-1996
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-169-077-1

Query Match          100.0%; Score 54; DB 15; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOKIKHVYK 11
DB 1 KOKIKHVYK 11

RESULT 4
US-09-424-292-4
; Sequence 4, Application US/09424292
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: Improved Delivery of Disease Modifiers
; FILE REFERENCE: 205375
; CURRENT APPLICATION NUMBER: US/09/424,292
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: PCT/CA98/00448
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: CA 2,205,771
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 4
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-424-292-4

Query Match          100.0%; Score 54; DB 18; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOKIKHVYK 11
DB 1 KOKIKHVYK 11

RESULT 5
US-09-685-010-30
; Sequence 30, Application US/09685010
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A.
; APPLICANT: Cruz, Tony F.
```

```

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: CELLULAR RESPONSE TO INJURY AND OTHER PROLIFERATING CELL
; FILE REFERENCE: 910130.401C1
; CURRENT APPLICATION NUMBER: US/09/685,010
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide composition that binds a hyalauronan
US-09-685-010-30

Query Match          100.0%; Score 54; DB 20; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KOKIKHVYK 11
        |||
Db      1 KOKIKHVYK 11

RESULT 6
; Sequence 30, Application US/09978309A
; GENERAL INFORMATION:
; APPLICANT: Cruz, Tony
; APPLICANT: Pastrak, Aleksandra
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
; FILE REFERENCE: 033352-010
; CURRENT APPLICATION NUMBER: US/09/978,309A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 09/685,010
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/541,522
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/127,457
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 30
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide composition that binds a hyalauronan
US-09-978-309A-30

Query Match          100.0%; Score 54; DB 23; Length 11;
Best Local Similarity 100.0%; Pred. No. 0.0071;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KOKIKHVYK 11
        |||
Db      1 KOKIKHVYK 11

RESULT 7
; Sequence 7, Application US/09424292
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: Improved Delivery of Disease Modifiers
; FILE REFERENCE: 205375
; CURRENT APPLICATION NUMBER: US/09/424,292
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: PCT/CA98/00448
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; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: CA 2,205,771
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: patentin version 3.1
; SEQ ID NO 7
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-424-292-7

Query Match          90.7%; Score 49; DB 18; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.052;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KOKIKHVYK 10
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Db      1 KOKIKHVYK 10

RESULT 8
; Sequence 30, Application US/08318892B
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR FOR
; TITLE OF INVENTION: HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING PEPTID
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,892B
; FILING DATE: 1-DEC-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pierri, Margaret A
; REGISTRATION NUMBER: 30709
; REFERENCE/DOCKET NUMBER: STM-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-892B-30

Query Match          83.3%; Score 45; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KOKIKHVYK 9
        |||
Db      1 KOKIKHVYK 9

RESULT 9
; Sequence 30, Application US/08318892B
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: Improved Delivery of Disease Modifiers
; FILE REFERENCE: 205375
; CURRENT APPLICATION NUMBER: US/09/424,292
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: PCT/CA98/00448
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; Sequence 60, Application US/09685010
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A.
; APPLICANT: Cruz, Tony F.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
; TITLE OF INVENTION: CELLULAR RESPONSE TO INJURY AND OTHER PROLIFERATING CELL
; FILE REFERENCE: 910130.401C1
; CURRENT APPLICATION NUMBER: US/09/685,010
; CURRENT FILING DATE: 2001-05-23
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-685-010-60

Query Match      83.3%; Score 45; DB 20; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 KOKIKHVVK 9
Db      1 KOKIKHVVK 9

RESULT 10
US-09-978-309A-60
; Sequence 60, Application US/09978309A
; GENERAL INFORMATION:
; APPLICANT: Cruz, Tony
; APPLICANT: Pastirak, Aleksandra
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
; TITLE OF INVENTION: Hyaladerlin and Hyaluronans
; FILE REFERENCE: 033352-010
; CURRENT APPLICATION NUMBER: US/09/978,309A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 09/685,010
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/541,522
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/127,457
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-978-309A-60

Query Match      83.3%; Score 45; DB 23; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 KOKIKHVVK 9
Db      1 KOKIKHVVK 9

RESULT 11
US-08-318-892B-31
; Sequence 31, Application US/08318892B
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM - RECEPTOR FOR
; TITLE OF INVENTION: HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING PEPTIDES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESS: c/o FISH & NEAVE
```

```
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,892B
; FILING DATE: 1-DEC-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pierri, Margaret A
; REGISTRATION NUMBER: 30709
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 31:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-318-892B-31
```

```
Query Match      81.5%; Score 44; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3 KIKHVVKLK 11
Db      1 KIKHVVKLK 9
```

```
RESULT 12
US-09-424-292-8
; Sequence 8, Application US/09424292
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: Improved delivery of Disease Modifiers
; FILE REFERENCE: 205375
; CURRENT APPLICATION NUMBER: US/09/424,292
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: PCT/CA98/00448
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: CA 2,205,771
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-424-292-8
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Query Match      75.9%; Score 41; DB 18; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.5;
Matches 8; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      1 KOKIKHVVKL 10
Db      1 KOKIEHVVEL 10

RESULT 13
US-09-424-292-11
```


Sequence 31, Application US/09424292
GENERAL INFORMATION:
APPLICANT: Turley, Eva A
TITLE OF INVENTION: Improved Delivery of Disease Modifiers
FILE REFERENCE: 205375
CURRENT APPLICATION NUMBER: US/09/424,292
CURRENT FILING DATE: 2000-07-06
PRIOR APPLICATION NUMBER: PCT/CA98/00448
PRIOR FILING DATE: 1998-05-11
PRIOR APPLICATION NUMBER: CA 2,205,771
PRIOR FILING DATE: 1997-05-22
NUMBER OF SEQ ID NOS: 36
SOFTWARE: PatentIn version 3.1
SEQ ID NO 11
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-424-292-11

Query Match 63.0%; Score 34; DB 18; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.2e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 IKHVYKL 10
|||
Db 1 IKHVYKL 7

RESULT 14
US-08-474-654-29
Sequence 29, Application US/08474654
GENERAL INFORMATION:
APPLICANT: Natori, Shunji
APPLICANT: Takahashi, Haruo
APPLICANT: Kobayashi, Yohei
APPLICANT: Hoshino, Masaharu
TITLE OF INVENTION: NOVEL POLYPEPTIDE AND USE THEREOF
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue
CITY: N.W.
STATE: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,654
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP Hei-6-268723
FILING DATE: 01-NOV-1994
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /note="The carboxyl terminus is a
OTHER INFORMATION: carbamoyl group."
US-08-474-654-29

Query Match 57.4%; Score 31; DB 8; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVYKLK 11
|||
Db 1 KIKHVYKLK 9

RESULT 15
US-08-474-654-39
Sequence 39, Application US/08474654
GENERAL INFORMATION:
APPLICANT: Natori, Shunji
APPLICANT: Takahashi, Haruo
APPLICANT: Kobayashi, Yohei
APPLICANT: Hoshino, Masaharu
TITLE OF INVENTION: NOVEL POLYPEPTIDE AND USE THEREOF
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sughrue, Mion, Zinn, Macpeak & Seas
STREET: 2100 Pennsylvania Avenue
CITY: N.W.
STATE: Washington D.C.
COUNTRY: U.S.A.
ZIP: 20037-3202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,654
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP Hei-6-268723
FILING DATE: 01-NOV-1994
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-474-654-39

Query Match 57.4%; Score 31; DB 8; Length 9;
Best Local Similarity 77.8%; Pred. No. 4.2e+06;
Matches 7; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 KIKHVYKLK 11
|||
Db 1 KIKHVYKLK 9

Search completed: February 8, 2003, 11:01:45
Job time : 133 secs

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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:58:17 ; Search time 18 Seconds

(without alignments)
49,548 Million cell updates/sec

Title: US-09-685-010-30

Perfect score: 54

Sequence: 1 KQKIKHVKK 11

Scoring table: BLOSUM62

Searched: 405691 seqs, 81078759 residues

Total number of hits satisfying chosen parameters: 123350

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Pending Parents_AA_New:*
1: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	31	57.4	9	6	US-10-133-210-263
2	27	50.0	10	6	US-10-083-259-11
3	24	44.4	8	6	US-10-189-437-69
4	24	44.4	9	6	US-10-211-086-284
5	23	42.6	8	5	US-09-641-528-19345
6	23	42.6	8	5	US-09-641-528-19345
7	23	42.6	9	5	US-09-641-528-9809
8	23	42.6	9	5	US-09-641-528-33056
9	23	42.6	9	5	US-09-641-528-40827
10	23	42.6	9	5	US-09-641-528-9809
11	23	42.6	9	5	US-09-641-528-33056
12	23	42.6	9	5	US-09-641-528-40827
13	23	42.6	10	5	US-09-641-528-406
14	23	42.6	10	5	US-09-641-528-12718
15	23	42.6	10	5	US-09-641-528-25627
16	23	42.6	10	5	US-09-641-528-33057
17	23	42.6	10	5	US-09-641-528-406
18	23	42.6	10	5	US-09-641-528-12718
19	23	42.6	10	5	US-09-641-528-25627
20	23	42.6	10	5	US-09-641-528-33057
21	23	42.6	11	5	US-09-641-528-3545
22	23	42.6	11	5	US-09-641-528-9742
23	23	42.6	11	5	US-09-641-528-19346
24	23	42.6	11	5	US-09-641-528-25429
25	23	42.6	11	5	US-09-641-528-25628
26	23	42.6	11	5	US-09-641-528-30930

27	23	42.6	11	5	US-09-641-528-32779	Sequence 32779, A
28	23	42.6	11	5	US-09-641-528-33058	Sequence 33058, A
29	23	42.6	11	5	US-09-641-528-40663	Sequence 40663, A
30	23	42.6	11	5	US-09-641-528-3545	Sequence 3545, Ap
31	23	42.6	11	5	US-09-641-528-9742	Sequence 9742, Ap
32	23	42.6	11	5	US-09-641-528-19346	Sequence 19346, A
33	23	42.6	11	5	US-09-641-528-25429	Sequence 25429, A
34	23	42.6	11	5	US-09-641-528-25628	Sequence 25628, A
35	23	42.6	11	5	US-09-641-528-30930	Sequence 30930, A
36	23	42.6	11	5	US-09-641-528-32779	Sequence 32779, A
37	23	42.6	11	5	US-09-641-528-33058	Sequence 33058, A
38	23	42.6	11	5	US-09-641-528-40663	Sequence 40663, A
39	22	40.7	8	5	US-09-390-225B-28	Sequence 28, Appl
40	22	40.7	8	5	US-09-641-528-9824	Sequence 9824, Ap
41	22	40.7	8	5	US-09-641-528-33147	Sequence 33147, A
42	22	40.7	8	5	US-09-641-528-40879	Sequence 40879, A
43	22	40.7	8	5	US-09-641-528-9824	Sequence 9824, Ap
44	22	40.7	8	5	US-09-641-528-33147	Sequence 33147, A
45	22	40.7	8	5	US-09-641-528-40879	Sequence 40879, A

ALIGNMENTS

```
RESULT 1
US-10-133-210-263
; Sequence 263, Application US/10133210
; GENERAL INFORMATION:
; APPLICANT: Delisl, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulikorta, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiqing
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 263
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-263
Query Match 57.4%; Score 31; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 3.3e+05;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 1 KOKIKHV 8
1 | | | | |
Db 1 KIKIKHV 8
;
RESULT 2
US-10-083-259-11
; Sequence 11, Application US/10083259
; GENERAL INFORMATION:
; APPLICANT: Nielsen, Peter E.
; APPLICANT: Gierman, Birgit Kjaeldgaard
; APPLICANT: Good, Liam
; APPLICANT: Hansen, Henrik Frydenlund
; APPLICANT: Beck, Frederik
; APPLICANT: Malik, Lella
; APPLICANT: Schou, Carsten
; APPLICANT: Wissenbach, Margit
; TITLE OF INVENTION: Modified Peptide Nucleic Acid (PNA) Molecules
; FILE REFERENCE: PANT-0301
; CURRENT APPLICATION NUMBER: US/10/083,259
```

```
; CURRENT FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: 09/689,155
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 160
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 11
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Construct
US-10-083-259-11
```

```
Query Match          50.0%; Score 27; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      1 KKKIKHYVK 9
        1 1 1 1 1 1
Db      1 KKKVKEHYVK 9
```

```
RESULT 3
US-10-189-437-69
; Sequence 69, Application US/10189437
; GENERAL INFORMATION:
; APPLICANT: BOGGOCH, SAMUEL
; APPLICANT: BOGGOCH, ELENORE S.
; TITLE OF INVENTION: REPLICIN PEPTIDES AND ANTIBODIES THEREFORE
; FILE REFERENCE: 09425/46905
; CURRENT APPLICATION NUMBER: US/10/189,437
; CURRENT FILING DATE: 2002-07-08
; PRIOR APPLICATION NUMBER: 10/105,232
; PRIOR FILING DATE: 2002-03-26
; PRIOR APPLICATION NUMBER: 09/984,057
; PRIOR FILING DATE: 2001-10-26
; PRIOR APPLICATION NUMBER: 60/303,396
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: 60/278,761
; PRIOR FILING DATE: 2001-03-27
; NUMBER OF SEQ ID NOS: 729
; SOFTWARE: PatentIn 2.1
; SEQ ID NO: 69
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-189-437-69
```

```
Query Match          44.4%; Score 24; DB 6; Length 8;
Best Local Similarity 71.4%; Pred. No. 3.3e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      3 KKKHYVK 9
        1 1 1 1 1 1
Db      1 KKKHYVK 7
```

```
RESULT 4
US-10-211-088-284
; Sequence 284, Application US/10211088
; GENERAL INFORMATION:
; APPLICANT: Bright, Gary R.
; APPLICANT: Premkumar, D. David
; APPLICANT: Chen, Yih-Tai
; TITLE OF INVENTION: Novel Fusion Proteins And Assays For Molecular Binding
; FILE REFERENCE: 01-1022-US
; CURRENT APPLICATION NUMBER: US/10/211,088
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: 60/309,395
; PRIOR FILING DATE: 2001-08-01
; PRIOR APPLICATION NUMBER: 60/341,589
; PRIOR FILING DATE: 2001-12-13
; NUMBER OF SEQ ID NOS: 366
```

```
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 284
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Nuclear localization signal
US-10-211-088-284
```

```
Query Match          44.4%; Score 24; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 3.3e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KKKIKH 6
        1 1 1 1 1
Db      4 KYKLKH 9
```

```
RESULT 5
US-09-641-528-19345
; Sequence 19345, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.010001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 19345
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-19345
```

```
Query Match          42.6%; Score 23; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 3.3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 KKKIKHV 7
        1 1 1 1 1 1
Db      2 KEYIRHV 8
```

```
RESULT 6
US-09-641-528A-19345
; Sequence 19345, Application US/09641528A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.010001
; CURRENT APPLICATION NUMBER: US/09/641,528A
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
```

```
; SEQ ID NO: 19345
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528A-19345
```

```
Query Match          42.6%; Score 23; DB 5; Length 8;
Best Local Similarity 57.1%; Pred. No. 3.3e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 KKKHVKK 7
    1: 1:1
Db 2 KKKHVKK 8
```

```
RESULT 7
US-09-641-528-9809
; Sequence 9809, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060 0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9809
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-9809
```

```
Query Match          42.6%; Score 23; DB 5; Length 9;
Best Local Similarity 44.4%; Pred. No. 3.3e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 KKKHVKK 11
    :: 1:1
Db 1 OVLHVKKR 9
```

```
RESULT 8
US-09-641-528-33056
; Sequence 33056, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060 0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33056
```

```
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-33056
```

```
Query Match          42.6%; Score 23; DB 5; Length 9;
Best Local Similarity 44.4%; Pred. No. 3.3e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 KKKHVKK 11
    :: 1:1
Db 1 OVLHVKKR 9
```

```
RESULT 9
US-09-641-528-40827
; Sequence 40827, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060 0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40827
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-40827
```

```
Query Match          42.6%; Score 23; DB 5; Length 9;
Best Local Similarity 44.4%; Pred. No. 3.3e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 3 KKKHVKK 11
    :: 1:1
Db 1 OVLHVKKR 9
```

```
RESULT 10
US-09-641-528A-9809
; Sequence 9809, Application US/09641528A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060 0100001
; CURRENT APPLICATION NUMBER: US/09/641,528A
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9809
; LENGTH: 9
```

```
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528A-9809
```

```
Query Match          42.6%; Score 23; DB 5; Length 9;
Best Local Similarity 44.4%; Pred. No. 3.3e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 3 KIKHVVKLK 11
   ::||:| |
Db 1 QVLHVLRK 9
```

```
RESULT 11
US-09-641-528A-33056
; Sequence 33056, Application US/09641528A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528A
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 33056
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528A-33056
```

```
Query Match          42.6%; Score 23; DB 5; Length 9;
Best Local Similarity 44.4%; Pred. No. 3.3e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 3 KIKHVVKLK 11
   ::||:| |
Db 1 QVLHVLRK 9
```

```
RESULT 12
US-09-641-528A-40827
; Sequence 40827, Application US/09641528A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528A
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 40827
; LENGTH: 9
; TYPE: PRT
```

```
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528A-40827
```

```
Query Match          42.6%; Score 23; DB 5; Length 9;
Best Local Similarity 44.4%; Pred. No. 3.3e+05;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
Oy 3 KIKHVVKLK 11
   ::||:| |
Db 1 QVLHVLRK 9
```

```
RESULT 13
US-09-641-528-406
; Sequence 406, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 406
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-406
```

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Query Match          42.6%; Score 23; DB 5; Length 10;
Best Local Similarity 44.4%; Pred. No. 1.7e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
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```
Oy 3 KIKHVVKLK 11
   ::||:| |
Db 1 QVLHVLRK 9
```

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RESULT 14
US-09-641-528-12718
; Sequence 12718, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12718
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-12718

Query Match          42.6%; Score 23; DB 5; Length 10;
Best Local Similarity 44.4%; Pred. NO. 1.7e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3 KIKHVYK 11
      :: ||:| |
Db       1 QVLAHVLRK 9

RESULT 15
US-09-641-528-25627
; Sequence 25627, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDICING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 25627
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-25627

Query Match          42.6%; Score 23; DB 5; Length 10;
Best Local Similarity 44.4%; Pred. NO. 1.7e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      3 KIKHVYK 11
      :: ||:| |
Db       1 QVLAHVLRK 9

Search completed: February 8, 2003, 11:02:10
Job time : 19 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 8, 2003, 10:57:16 : Search time 14 Seconds
(without alignments)
23.118 Million cell updates/sec

Title: US-09-685-010-30
Perfect score: 54
Sequence: 1 K0KIKHVYK 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 83753

Minimum DB seq length: 0
Maximum DB seq length: 11

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*
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3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep.*
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6: /cgn2_6/ptodata/1/1aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	46.3	8	4	US-08-477-928A-47
2	24	44.4	10	4	US-09-019-346A-5
3	23	42.6	7	4	US-07-861-458C-139
4	23	42.6	11	1	US-08-193-521-1
5	23	42.6	11	1	US-08-434-120-95
6	23	42.6	11	1	US-08-465-325-94
7	23	42.6	11	4	US-09-115-737-94
8	22	40.7	9	4	US-09-644-600-34
9	22	40.7	9	4	US-09-644-600-65
10	22	40.7	10	1	US-08-097-830E-16
11	22	40.7	10	2	US-08-456-112B-16
12	22	40.7	11	1	US-08-465-325-151
13	22	40.7	11	4	US-09-115-737-151
14	21	38.9	8	1	US-07-924-054-6
15	21	38.9	9	4	US-08-584-043A-3
16	21	38.9	10	4	US-08-584-043A-4
17	21	38.9	11	4	US-08-584-043A-5
18	20	37.0	5	1	US-08-240-514-11
19	20	37.0	5	2	US-08-612-302A-11
20	20	37.0	5	4	US-08-974-549A-122
21	20	37.0	7	2	US-08-869-506-11
22	20	37.0	7	2	US-08-790-912-8
23	20	37.0	7	3	US-09-128-967-11
24	20	37.0	8	1	US-08-594-447-5
25	20	37.0	8	1	US-08-541-964-4
26	20	37.0	8	2	US-08-621-803-166
27	20	37.0	8	2	US-08-621-259A-133

28	20	37.0	8	2	US-08-665-647-19	Sequence 19, App1
29	20	37.0	8	2	US-09-016-366A-36	Sequence 36, App1
30	20	37.0	8	4	US-09-288-061-2	Sequence 2, App1
31	20	37.0	8	4	US-09-217-352-166	Sequence 166, App
32	20	37.0	8	5	PCT-US95-09262-133	Sequence 133, App
33	20	37.0	9	2	US-08-621-803-160	Sequence 160, App
34	20	37.0	9	2	US-08-621-803-161	Sequence 161, App
35	20	37.0	9	2	US-08-621-803-195	Sequence 195, App
36	20	37.0	9	2	US-08-621-259A-127	Sequence 127, App
37	20	37.0	9	2	US-08-621-259A-128	Sequence 128, App
38	20	37.0	9	4	US-09-217-352-160	Sequence 160, App
39	20	37.0	9	4	US-09-217-352-161	Sequence 161, App
40	20	37.0	9	4	US-09-217-352-195	Sequence 195, App
41	20	37.0	9	5	PCT-US95-09262-127	Sequence 127, App
42	20	37.0	9	5	PCT-US95-09262-128	Sequence 128, App
43	20	37.0	10	2	US-08-621-803-156	Sequence 156, App
44	20	37.0	10	2	US-08-621-803-157	Sequence 157, App
45	20	37.0	10	2	US-08-621-259A-123	Sequence 123, App

ALIGNMENTS

RESULT 1
US-08-477-928A-47
Sequence 47, Application US/08477928A
Patent No. 6207389
GENERAL INFORMATION:
APPLICANT: Dosch, Hans M.
TITLE OF INVENTION: METHODS FOR CONTROLLING T
TITLE OF INVENTION: LYMPHOCYTE MEDIATED IMMUNE RESPONSES
NUMBER OF SEQUENCES: 49
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTTS
STREET: 1299 Pennsylvania Avenue
CITY: Washington D.C.
STATE: California
COUNTRY: U.S.A.
ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,928A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36902
REFERENCE/DOCKET NUMBER: 19060-0105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 639 7700
TELEFAX: (202) 639 7890
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-477-928A-47

Query Match 46.3% Score 25; DB 4; Length 8;
Best Local Similarity 66.7%; Pred. No. 2e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 KIKHV 8
1:1:1
DB 3 KIKHV 8

RESULT 2
US-09-019-346A-5
; Sequence 5, Application US/09019346A
; Patent No. 6372720
; GENERAL INFORMATION:
; APPLICANT: Longmuir, Kenneth J.
; APPLICANT: Waring, Alan J.
; APPLICANT: Haynes, Sherry M.
; TITLE OF INVENTION: Liposome Fusion and Delivery Vehicle
; FILE REFERENCE: A65189/RPT/DAV
; CURRENT APPLICATION NUMBER: US/09/019,346A
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HIV-1 matrix protein
US-09-019-346A-5

Query Match 44.4%; Score 24; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 KOKIH 6
1 : 1 : 1
Db 5 KYKLKH 10

RESULT 3
US-07-861-458C-139
; Sequence 139, Application US/07861458C
; Patent No. 6232061
; GENERAL INFORMATION:
; APPLICANT: Marchionni, Mark Andrew
; APPLICANT: Johnson, Karl D.
; TITLE OF INVENTION: HOMOLOG CLONING
; NUMBER OF SEQUENCES: 142
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/861,458C
; FILING DATE: 04/01/92
; CLASSIFICATION: 435
; PRIOR APPLICATION NUMBER:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 04585/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 139:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7
; TYPE: amino acid
; TOPOLOGY: linear
US-07-861-458C-139

Query Match 42.6%; Score 23; DB 4; Length 7;

Best Local Similarity 80.0%; Pred. No. 2e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 4 IKHVV 8
1 : 1 : 1
Db 2 KKHVV 6

RESULT 4
US-08-193-521-1
; Sequence 1, Application US/08193521
; Patent No. 5470950
; GENERAL INFORMATION:
; APPLICANT: Maloy, W. Lee
; APPLICANT: Karl, U. Prasad
; APPLICANT: Williams, Jon I.
; TITLE OF INVENTION: Biologically Active Peptide
; TITLE OF INVENTION: Compositions and Uses Therefor
; NUMBER OF SEQUENCES: 19
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carella, Byrne, Bain, Gillfillan,
; ADDRESSEE: Cecchi & Stewart
; STREET: 6 Becker Farm Road
; CITY: Roseland
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07068
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; COMPUTER: IBM PS/2
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: DW4.V2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/193,521
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/870,960
; FILING DATE:
; APPLICATION NUMBER: 07/760,054
; FILING DATE: 13-SEP-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Olstein, Elliot M.
; REGISTRATION NUMBER: 24,025
; REFERENCE/DOCKET NUMBER: 421250-161
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-994-1700
; TELEFAX: 201-994-1744
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; OTHER INFORMATION: May be a C-terminal amide,
; OTHER INFORMATION: and/or may be acetylated at
; OTHER INFORMATION: N-terminus.
US-08-193-521-1

Query Match 42.6%; Score 23; DB 1; Length 11;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 OKIKHVAKL 10
1 : 1 : 1 : 1
Db 2 KKLKLIKLT 10

RESULT 5
US-08-434-120-95
; Sequence 95, Application US/08434120

Patent No. 5635479
GENERAL INFORMATION:
APPLICANT: Baker, Margaret A.
APPLICANT: Jacob, Leonard S.
APPLICANT: Maloy, W. Lee
TITLE OF INVENTION: Treatment of Gynecological
TITLE OF INVENTION: Malignancies with
TITLE OF INVENTION: Biologically Active Peptides
NUMBER OF SEQUENCES: 117
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Carella, Byrne, Bain, Gilfillan,
STREET: 6 Becker Farm Road
CITY: Roseland
STATE: New Jersey
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: DM4.V2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,120
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/297,950
FILING DATE:
APPLICATION NUMBER: US/08/226,108
FILING DATE:
APPLICATION NUMBER: US/07/937,462
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Olstein, Elliot M.
REGISTRATION NUMBER: 24,025
REFERENCE/DOCKET NUMBER: 421250-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 95:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-434-120-95

Query Match 42.6%; Score 23; DB 1; Length 11;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 OKIKHYKL 10
:11::11
DB 2 KIKKLKL 10

RESULT 6
US-08-465-325-94
Sequence 94, Application US/08465325
Patent No. 5686563
GENERAL INFORMATION:
APPLICANT: Magalini Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: Plymouth Meeting, PA 19462
TITLE OF INVENTION: Biologically Active Peptides Having
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I. Street, N.W. Suite 700

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,325
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0021-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4000
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-325-94

Query Match 42.6%; Score 23; DB 1; Length 11;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 OKIKHYKL 10
:11::11
DB 2 KIKKLKL 10

RESULT 7
US-09-115-737-94
Sequence 94, Application US/09115737
Patent No. 6348445
GENERAL INFORMATION:
APPLICANT: U. Prasad Karl
Taffy J. Williams
Michael McLane
TITLE OF INVENTION: Biologically Active Peptides With Reduced
Toxicity in Animals and a Method for Preparing Same
NUMBER OF SEQUENCES: 156
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner, L.L.P.
STREET: 1300 I Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,737
FILING DATE: 15-Jul-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/465,330
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387,0021-06000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 94:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 94:
US-09-115-737-94

Query Match 42.6%; Score 23; DB 4; Length 11;
Best Local Similarity 44.4%; Pred. NO. 2.9e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 OKIKHVKL 10
:|:|:|
Db 2 KKKKLKL 10

RESULT 8
US-09-644-600-34
Sequence 34, Application US/09644600
Patent No. 6451500
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoishi
TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO: 34
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 119-127 of the TADG-15 protein
US-09-644-600-34

Query Match 40.7%; Score 22; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. NO. 2e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KIKHVKL 10
:|:|:|
Db 1 KVKDALKL 8

RESULT 9
US-09-644-600-65
Sequence 65, Application US/09644600
Patent No. 6451500
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
APPLICANT: Tanimoto, Hirotoishi

TITLE OF INVENTION: TADG-15: An Extracellular Serine Protease
FILE REFERENCE: D6064CIP/D
CURRENT APPLICATION NUMBER: US/09/644,600
CURRENT FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/421,213
PRIOR FILING DATE: 1999-10-20
PRIOR APPLICATION NUMBER: 09/027,337
PRIOR FILING DATE: 1998-02-20
NUMBER OF SEQ ID NOS: 98
SEQ ID NO: 65
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: Residues 119-127 of the TADG-15 protein
US-09-644-600-65

Query Match 40.7%; Score 22; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. NO. 2e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KIKHVKL 10
:|:|:|
Db 1 KVKDALKL 8

RESULT 10
US-08-097-830E-16
Sequence 16, Application US/08097830E
Patent No. 5652211
GENERAL INFORMATION:
APPLICANT: Porro, Massimo
TITLE OF INVENTION: Peptides for Neutralizing The
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hedman, Gibson & Costigan, P.C.
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
COMPUTER: IBM PS/2
OPERATING SYSTEM: DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,830E
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Costigan, James V.
REGISTRATION NUMBER: 25,669
REFERENCE/DOCKET NUMBER: 576-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 302-8989
TELEFAX: (212) 302-8998
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: circular
FEATURE:
OTHER INFORMATION: sulfide bond between Cys and Cys
US-08-097-830E-16

Query Match 40.7%; Score 22; DB 1; Length 10;
Best Local Similarity 55.6%; Pred. NO. 3.9e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KIKHVVKLK 11
1:1:111
Db 1 KIKCKLK 9

RESULT 11
US-08-456-112B-16
; Sequence 16, Application US/08456112B
; Patent No. 5834430
; GENERAL INFORMATION:
; APPLICANT: Porto, Massimo
; TITLE OF INVENTION: POTENTIATION OF ANTIBIOTICS
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hedman, Gibson & Costigan
; STREET: 1185 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; OPERATING SYSTEM: DOS
; SOFTWARE: Word Perfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/456,112B
; FILING DATE: May 31, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Costigan, James V.
; REGISTRATION NUMBER: 25,669
; REFERENCE/DOCKET NUMBER: 576-004
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 302-8989
; TELEFAX: (212) 302-8998
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: circular
US-08-456-112B-16

Query Match 40.7%; Score 22; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 KIKHVVKLK 11
1:1:111
Db 1 KIKCKLK 9

RESULT 12
US-08-465-325-151
; Sequence 151, Application US/08465325
; Patent No. 5686563
; GENERAL INFORMATION:
; APPLICANT: Magalini Pharmaceuticals Inc.
; APPLICANT: 5110 Campus Drive
; APPLICANT: Plymouth Meeting, PA 19462
; TITLE OF INVENTION: Biologically Active Peptides Having
; TITLE OF INVENTION: N-Terminal Substitutions
; NUMBER OF SEQUENCES: 153
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I. Street, N.W. Suite 700
; CITY: Washington

STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,325
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0021-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-325-151

Query Match 40.7%; Score 22; DB 1; Length 11;
Best Local Similarity 40.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

OY 1 KOKIKHVVKL 10
1:1:111
Db 2 KKLKELK 11

RESULT 13
US-09-115-737-151
; Sequence 151, Application US/09115737
; Patent No. 6348445
; GENERAL INFORMATION:
; APPLICANT: U. Prasad Kari
; APPLICANT: Taffy J. Williams
; APPLICANT: Michael McLane
; TITLE OF INVENTION: Biologically Active Peptides With Reduced
; TITLE OF INVENTION: Toxicity in Animals and a Method for Preparing Same
; NUMBER OF SEQUENCES: 156
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner, L.L.P.
; STREET: 1300 I Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,737
; FILING DATE: 15-JUL-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,330

FILING DATE: 05-JUN-1995
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387,0021-06000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 151:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 151:
US-09-115-737-151

Query Match 40.7%; Score 22; DB 4; Length 11;
Best Local Similarity 40.0%; Pred. No. 4.3e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 KOKIKHVKL 10
I : I : I :
DB 2 KKLKELKL 11

RESULT 14
US-07-924-054-6
Sequence 6, Application US/07924054
Patent No. 5486472

GENERAL INFORMATION:
APPLICANT: SUZUKI, NO. 5486472uhlro
APPLICANT: KITADA, Chieko
APPLICANT: TSUDA, Masao
TITLE OF INVENTION: ANTIBODY TO PACAP AND USE THEREOF
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN, DIKE, BRONSTEIN, ROBERTS&
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/924,054
FILING DATE: 19920903
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: RESNICK, David S
REGISTRATION NUMBER: 34235
REFERENCE/DOCKET NUMBER: 40805
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-924-054-6

Query Match 38.9%; Score 21; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 1 KOKIKH 6
I : I :
DB 2 KQKVKH 7

RESULT 15
US-08-584-043A-3
Sequence 3, Application US/08584043A
Patent No. 6344436

GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
APPLICANT: Sparrow, James T.
APPLICANT: Hauer, Jochen
APPLICANT: Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
STATE: Los Angeles
COUNTRY: U.S.A.
ZIP: 90071-2066

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/584,043A
FILING DATE: January 8, 1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Warburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-584-043A-3

Query Match 38.9%; Score 21; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 2e+05;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 KOKIKHVK 9
I : I : I : I :
DB 1 KKKKKVTK 9

Search completed: February 8, 2003, 10:59:26
Job time : 15 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 11:02:17 ; Search time 14 Seconds
(without alignments)
69.667 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KLSQQLVKKR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 1100

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	34.8	4	2	140870	phospholipase C (B	
2	32.6	9	2	I54579	gene NF2 protein -	
3	32.6	10	2	A42089	transcription factor	
4	32.6	10	2	C54226	light-harvesting p	
5	30.4	9	1	YFPG	thymic factor - p	
6	30.4	9	2	A60957	thymocyte growth p	
7	30.4	9	2	S15850	vitamin D3 26-mono	
8	30.4	10	2	S28055	cytochrome b559 co	
9	30.4	10	2	P00784	NADH2 dehydrogenase	
10	28.3	6	2	S11024	hydrogen sulfite re	
11	28.3	6	2	A37765	hypothetical prote	
12	28.3	6	2	I48126	alpha-tubulin - Ch	
13	28.3	7	2	S55548	meib protein - Esc	
14	28.3	8	2	P0162	paramyosin - north	
15	28.3	9	2	A60108	exotoxin A - Strept	
16	28.3	9	2	S10920	venom protein HR-3	
17	28.3	10	2	D37397	hypothetical prote	
18	28.3	10	2	S09387	PV1 protein - huma	
19	28.3	10	2	C39111	Ig heavy chain C r	
20	28.3	10	2	S71948	matrix metalloprot	
21	28.3	10	2	EX0660	lysosome-associate	
22	26.1	5	2	T14910	hypothetical prote	
23	26.1	6	2	S02617	alcohol dehydrogen	
24	26.1	7	2	S57274	triacylglycerol 11	
25	26.1	7	2	PS0254	18k protein 5507 -	
26	26.1	8	2	I64832	Ca2+-transporting	
27	26.1	9	2	S13333	alpha/beta-gliadin	
28	26.1	9	2	S78762	ribosomal protein	
29	26.1	9	2	PC7076	spectrin alpha cha	

30	12	26.1	9	2	I52974	seminal vesicle pr
31	12	26.1	10	2	S27178	neurokinin A-relat
32	12	26.1	10	2	S13324	viral protein - Agr
33	12	26.1	10	2	S70721	heat shock protein
34	11	23.9	6	2	A61419	sarcosine dehydrog
35	11	23.9	6	2	JH0784	neuropeptide YF-6
36	11	23.9	6	2	B33932	Ig mu chain D regi
37	11	23.9	7	2	S19630	ribosomal protein
38	11	23.9	7	2	A38671	peptidylglycine mo
39	11	23.9	8	1	LFSAWE	probable maza lead
40	11	23.9	8	2	PN0043	phosphatidylethano
41	11	23.9	8	2	S45651	probable Na+-trans
42	11	23.9	9	2	S30494	cat gene leader pe
43	11	23.9	9	2	B24362	chloramphenicol O-
44	11	23.9	9	2	S13889	phosphoenolpyruvat
45	11	23.9	9	2	PC2197	zymogen granule me

ALIGNMENTS

RESULT 1
I40870 phospholipase C (EC 3.1.4.3) - Clostridium perfringens (fragment)
C/Species: Clostridium perfringens
C/Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 21-Jul-2000
C/Accession: I40870
R/Toyonaga, T.; Matsushita, O.; Katayama, S.; Minami, J.; Okabe, A.
Microbiol. Immunol. 36, 603-613, 1992
A/Title: Role of the upstream region containing an intrinsic DNA curvature in the negativ
A/Reference number: I40870; MVID:9236045; PMID:1522810
A/Accession: I40870
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-4 <RES>
A/Cross-references: EMBL:X62825; NID:G40622; PIDD:CAA44636.1; PTD:G4377417
C/Genetics:
A/Genes: plc
A/Keywords: phosphoric diester hydrolase

Query Match 34.8%; Score 16; DB 2; Length 4;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VKRK 10
DB 1 MKRK 4
RESULT 2
I54379 gene NF2 protein - human (fragment)
C/Species: Homo sapiens (hmn)
C/Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 21-Jul-2000
C/Accession: I54379
R/Arai, E.; Ikeuchi, T.; Nakamura, Y.
Hum. Mol. Genet. 3, 937-939, 1994
A/Title: Characterization of the translocation breakpoint on chromosome 22q12.2 in a pati
A/Reference number: I54379; MVID:95038750; PMID:7551241
A/Accession: I54379
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-9 <RES>
A/Cross-references: GB:S75841; NID:G861532; PIDD:AAAD14190.1; PTD:G4261890
C/Genetics:
A/Genes: GDB:NF2
A/Cross-references: GDB:120232; OMIM:101000
A/Map position: 22q12.2-22q12.2

Query Match 32.6%; Score 15; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 KUKS 4
|||:
Db 4 KUKA 7

RESULT 3

A:Accession: A42089
transcription factor I-POU protein, alternative splice form - fruit fly (Drosophila mela
C:Species: Drosophila melanogaster
C:Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
R:Tracy, M.N.; Neilson, L.I.; Turner, E.E.; He, X.; Rosenfeld, M.G.
Cell 68, 491-505, 1992
A:Title: Twin of I-POU: a two amino acid difference in the I-POU homeodomain distinguish
A:Reference number: A42089; MUID:92154665; PMID:1346754
A:Accession: A42089
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-10 <TR>
A:Cross-references: GB:S82271; NID:9245517; PID:9245518
A:Note: sequence extracted from NCBI backbone (NCBIN:82267, NCBIP:82273)
C:Genetics:
A:Gene: PLYBase:Ipou
A:Cross-references: FlyBase:FBgn0004418

Query Match 32.6%; Score 15; DB 2; Length 10;
Best Local Similarity 100.0%; Pred.No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 KKK 10
|||:
Db 4 KKK 6

RESULT 4

CS4226
light-harvesting protein B-830 alpha-3 chain - Chromatium purpuratum (fragment)
C:Species: Chromatium purpuratum
C:Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
R:Kerfeld, C.A.; Yeates, T.O.; Thorner, J.P.
Biochemistry 33, 2178-2184, 1994
A:Title: Purification and characterization of the peripheral antenna of the purple-sulfu
A:Reference number: A54226; MUID:94162224; PMID:8117674
A:Accession: CS4226
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-10 <KER>
C:Keywords: antenna complex; light-harvesting polypeptide

Query Match 32.6%; Score 15; DB 2; Length 10;
Best Local Similarity 50.0%; Pred.No. 7.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 KSQLYK 8
|||:
Db 4 KANLVQ 9

RESULT 5

YFPG
thymic factor - pig (facteur thymique serique)
N:Alternate names: FTS (facteur thymique serique)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 13-Jul-1991 #sequence_revision 13-Jul-1991 #text_change 07-May-1999
R:Accession: A01523; A60983
R:Pleau, J.M.; Dardenne, M.; Blouquait, Y.; Bach, J.F.
J. Biol. Chem. 252, 8045-8047, 1977
A:Title: Structural study of circulating thymic factor: a peptide isolated from pig seru
A:Reference number: A01523; MUID:78026571; PMID:914862
A:Accession: A01523
A:Molecule type: protein
A:Residues: 1-9 <PLS>

R:Bach, J.F.; Dardenne, M.; Pleau, J.M.; Rosa, J.
Nature 266, 55-57, 1977
A:Title: Biochemical characterisation of a serum thymic factor.
A:Reference number: A60983; MUID:77123829; PMID:300146
A:Accession: A60983

A:Molecule type: protein
A:Residues: 2,2',2'',6-9 <BAC>
C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunosays.
C:Comment: See PIR:A60957 (sheep) for discussion of another possible N-terminal modificat
C:Superfamily: thymic factor
C:Keywords: pyroglutamic acid
P.I./Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 30.4%; Score 14; DB 1; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KSQ 5
|||:
Db 3 KSQ 5

RESULT 6

A60957
thymocyte growth peptide - sheep
N:Contains: FTS (facteur thymique serique)
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 24-Nov-1999
R:Accession: A60957
R:Ernstroem, U.; Gafvelin, G.; Rudja, J.M.
Biosci. Rep. 10, 403-412, 1990
A:Title: Purification of thymocyte growth peptide (TGP) from sheep thymus. Relationship t
A:Reference number: A60957; MUID:91064427; PMID:2249004
A:Accession: A60957

A:Molecule type: protein
A:Residues: 1-9 <ERN>
C:Comment: This peptide induces DNA synthesis in immature thymocytes, but not peripheral
in a variety of immunosays.
C:Comment: This peptide was isolated in two forms. One form contained the pyroglutamate c
r form (thymocyte growth peptide) contains a large, non-peptide blocking group with a hig
C:Superfamily: thymic factor
C:Keywords: blocked amino end; pyroglutamic acid (Glx) (in FTS) #status experimental
P.I./Modified site: pyroglutamate carboxylic acid (Glx) (in thymocyte growth peptide) #status experime
P.I./Modified site: blocked amino end (Glx) (in thymocyte growth peptide)

Query Match 30.4%; Score 14; DB 2; Length 9;
Best Local Similarity 100.0%; Pred.No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KSQ 5
|||:
Db 3 KSQ 5

RESULT 7

S15850
vitamin D3 26-monoxygenase (BC 1.14.14.-) cytochrome P450 27 - pig (fragment)
N:Alternate names: cytochrome P450(26); vitamin D3 26-hydroxylase
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 23-Apr-1993 #sequence_revision 23-Apr-1993 #text_change 05-Mar-1999
R:Accession: S15850
R:Bergman, T.; Postlind, H.
Biochem. J. 276, 427-432, 1991
A:Title: Characterization of mitochondrial cytochromes P-450 from pig kidney and liver c
A:Reference number: S15850; MUID:91264797; PMID:2049072
A:Accession: S15850
A:Molecule type: protein
A:Residues: 1-9 <BIO>
C:Genetics:
A:Gene: CYP27
C:Superfamily: unassigned cytochrome P450; cytochrome P450 homology
C:Keywords: heme; mitochondrion; monooxygenase; oxidoreductase; transmembrane protein

RESULT 13

SS5548
 mcrB protein - Escherichia coli (fragment)
 C/Species: Escherichia coli
 C/Date: 10-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 07-May-1999
 C/Accession: SS5548
 R/Kueger, T.; Wild, C.; Noyer-Weidner, M.
 EMBO J. 14, 2661-2669, 1995
 A/Title: MCRB: a prokaryotic protein specifically recognizing DNA containing modified cy
 A/Reference number: SS5548; MUID:95300799; PMID:7781618
 A/Accession: SS5548
 A/Molecule type: protein
 A/Residues: 1-7 <KKU>

Query Match 28.3%; Score 13; DB 2; Length 7;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 LVKRR 10

DB 1 LAMRK 5

RESULT 14

PL0162
 paramyosin - northern quahog (fragment)
 C/Species: Mercenaria mercenaria (northern quahog)
 C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 11-May-2000
 C/Accession: PL0162
 R/Matabe, S.; Tsuchiya, T.; Hartshorne, D.J.
 Comp. Biochem. Physiol. B 94, 813-821, 1989
 A/Title: Phosphorylation of paramyosin.
 A/Reference number: PL0162; MUID:90107385; PMID:2532591
 A/Accession: PL0162

A/Molecule type: protein
 A/Residues: 1-8 <MAT>
 A/Experimental source: white adductor muscle
 A/Note: the sequence is the phosphorylated tryptic peptide
 C/Comment: This protein is thought to exist as a dimer of two subunits, termed alpha-par
 om the carboxyl-terminal end of the molecule. Only alpha-paramyosin is phosphorylated by
 C/Keywords: muscle; phosphoprotein
 P/5/Binding site: phosphate (Ser) (covalent) #status experimental

Query Match 28.3%; Score 13; DB 2; Length 8;
 Best Local Similarity 42.9%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KSQLYKR 9

DB 2 RMSVSVR 8

RESULT 15

A60108
 exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)
 N/Alternate names: blastogen A; scarlet fever toxin
 C/Species: Streptococcus pyogenes
 C/Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 07-Feb-1997
 C/Accession: A60108
 R/Schlievert, P.M.; Gray, E.D.
 Infect. Immun. 57, 1865-1867, 1989
 A/Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blast
 A/Reference number: A60108; MUID:89254013; PMID:2498210
 A/Accession: A60108
 A/Molecule type: protein
 A/Residues: 1-9 <SCH>
 C/Keywords: exotoxin

Query Match 28.3%; Score 13; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 SQL_6

DB 6 SQL 8

Search completed: February 8, 2003, 11:04:21
 Job time : 14 secs

AC P31929;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE Unknown protein from 2d-page of liver tissue (Spot 106) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Liver;
 RX MEDLINE=94147969; PubMed=8113870;
 RA Hughes G.J., Frutiger S., Paquet N., Paeguali C., Sanchez J.-C.,
 RA Tlassot J.-D., Batroch A., Appel R.D., Hochertrasser D.F.;
 RT "Human liver protein map: update 1993."
 RL Electrophoresis 14:1216-1222(1993).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6, ITS MW IS: 15 KDa.
 DR SWISS-2DPAGE; P31929; HUMAN.
 FT NON TER
 SQ SEQUENCE 9 AA; 1129 MW; D02DF41B6D3322 CRC64;

Query Match 34.8%; Score 16; DB 1; Length 9;
 Best Local Similarity 60.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 LVKRR 10
 DB 1 LVKKQ 5

RESULT 3

TEMP RANTE
 ID TEMP RANTE STANDARD; PRT; 10 AA.
 AC P56923;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Temporin K.
 OS Rana temporaria (European common frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
 OX NCBI_TaxID=8407;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Skin;
 RX MEDLINE=97175050; PubMed=9022710;
 RA Simmaco M., Mignogna G., Canoteni S., Miele R., Mangoni M.L.,
 RA Bartra D.;
 RT "Temporins, antimicrobial peptides from the European red frog Rana
 RT temporaria."
 RL Eur. J. Biochem. 242:788-792(1996).
 CC -1- FUNCTION: HAS ANTIBACTERIAL ACTIVITY AGAINST GRAM-POSITIVE
 CC BACTERIA.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE BREVININ/ESCULENTIN/GAEGURIN/RUGOSIN
 CC FAMILY.
 KM Amphibian skin; Antibiotic; Amidation; Multigene family.
 FT MOD RES 10 10
 SQ SEQUENCE 10 AA; 1123 MW; 390549B337272457 CRC64;

Query Match 32.6%; Score 15; DB 1; Length 10;
 Best Local Similarity 80.0%; Pred. No. 3e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LKSQT 6
 DB 6 LKSL 10

RESULT 4

FARS_PANRE

ID FARS_PANRE STANDARD; PRT; 9 AA.
 AC P82661;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE 16-OCT-2001 (Rel. 40, Last annotation update)
 DE FMRamide-like neuropeptide PF5 (AMRNALVRF-amide).
 OS Panagrellus redivivus.
 CC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;
 CC Panagrolaimidae; Panagrolaimidae; Panagrellus.
 OX NCBI_TaxID=6233;
 RN [1]
 RP SEQUENCE, FUNCTION, AND AMIDATION.
 RA Wolff C.B., Marks N.D., Halcón D.W., Thomson D.P., Geary T.G.,
 RA Maule A.G.;
 RT "Isolation, characterization and pharmacology of FMRamide-related
 RT peptides (FARPs) from free-living nematode, Panagrellus redivivus."
 RL Submitted (JUL-2000) to the SWISS-PROT data bank.
 CC -1- FUNCTION: MYOACTIVE.
 CC -1- SIMILARITY: BELONGS TO THE FARP (FMRamide RELATED PEPTIDE)
 CC FAMILY.
 CC Neuropeptide; Amidation.
 FT MOD RES 9 9
 SQ SEQUENCE 9 AA; 1077 MW; A0D112C72DD45406 CRC64;

Query Match 30.4%; Score 14; DB 1; Length 9;
 Best Local Similarity 28.6%; Pred. No. 1.1e+05;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

OY 2 LKSQV 8
 DB 2 WRNALVR 8

RESULT 5

THYF PIG
 ID THYF PIG STANDARD; PRT; 9 AA.
 AC P01255;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 21-JUL-1986 (Rel. 01, Last annotation update)
 DE Thymic factor.
 OS Sus scrofa (Pig).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=78026571; PubMed=914862;
 RA Pleau J.-M., Dardenne M., Blouguet Y., Bach J.-F.;
 RT "Structural study of circulating thymic factor: a peptide isolated
 RT from pig serum. II. Amino acid sequence."
 RL J. Biol. Chem. 252:8045-8047(1977).
 CC -1- MISCELLANEOUS: THE BIOLOGICAL SOURCE(S) AND PHYSIOLOGICAL
 CC ACTIVITIES OF THIS PEPTIDE HAVE NOT BEEN DETERMINED.
 DR PIR; A01523; YEPG.
 FT MOD RES 1 1
 SQ SEQUENCE 9 AA; 876 MW; D50B87866C5B33D CRC64;

Query Match 30.4%; Score 14; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.1e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 KSQ 5
 DB 3 KSQ 5

RESULT 6

PSBF CAPAN
 ID PSBF CAPAN STANDARD; PRT; 10 AA.
 AC Q03367;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)

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DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Cytochrome B559 beta chain (Fragment).
GN PSBF.
OS Capsicum annuum (Bell pepper).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Capsicum.
OX NCBI_TaxId=4072;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=CV. Lamuyo; TISSUE=leaf, and Fruit;
RX MEDLINE=9309270; PubMed=1463853;
RA Kuntz M., Camara B., Weil J.-H., Schantz R.;
RT "The psbL gene from bell pepper (Capsicum annuum): plastid RNA
RT editing occurs in non-photosynthetic chromoplasts.";
RL Plant Mol. Biol. 20:1185-1188(1992)
CC -1- FUNCTION: THIS B-TYPE CYTOCHROME IS TIGHTLY ASSOCIATED WITH THE
CC REACTION CENTER OF PHOTOSYSTEM II AND POSSIBLY IS PART OF THE
CC WATER-OXIDATION COMPLEX.
CC -1- SUBUNIT: DIMER OF AN ALPHA AND A BETA CHAIN.
CC -1- SIMILARITY: BELONGS TO THE PSBE / PSBF FAMILY.
CC -----
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CC -----
DR EMBL; X65570; CAA46539.1; -.
DR InterPro: IPR001417; Cyt B559.
DR PROSITE: PS00537; CYTOCHROME B559; PARTIAL.
KM Chloroplast; Photosystem II; Heme; Electron transport; Transmembrane.
FT NON_TER 1 1
FT TRANSEM <1 10 BY SIMILARITY.
SQ SEQUENCE 10 AA; 1180 MW; 817D0F59D6D69DC5 CRC64;

Query Match 30.4%; Score 14; DB 1; Length 10;
Best Local Similarity 40.0%; Pred. No. 4.8e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLVKR 9
|::|
Db 6 QPIOR 10

RESULT 7
TKUL_UREUN STANDARD; PRT; 10 AA.
ID TKUL_UREUN
AC P40751;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Urechis tachykinin I.
DE Urechis uncinatus.
OC Eukaryota; Metazoa; Echinura; Xenopneusta; Urechidae; Urechis.
OX NCBI_TaxId=6432;
[1]
RN SEQUENCE AND SYNTHESIS.
RP TISSUE=ventral nerve cord;
RX MEDLINE=9323658; PubMed=8476410;
RA Ikeda T., Minakata H., Nomoto K., Kubota I., Muneka Y.;
RT "Two novel tachykinin-related neuropeptides in the echinoid worm,
RT Urechis uncinatus.";
RL Biochem. Biophys. Res. Commun. 192:1-6(1993).
CC -1- FUNCTION: CONTRACTILE ACTION ON THE INNER CIRCULAR BODY-WALL
CC MUSCLE OF THE ANIMAL.
CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
KM Tachykinin; Neuropeptide; Amidation.
FT MOD_RES 10 10 AMIDATION.
SQ SEQUENCE 10 AA; 1177 MW; C6D1C462C9D6C5A6 CRC64;

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Query Match 30.4%; Score 14; DB 1; Length 10;
Best Local Similarity 60.0%; Pred. No. 4.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KSQIV 7
|::|
Db 3 QSQFV 7

RESULT 8
FARL_ASCSU STANDARD; PRT; 7 AA.
ID FARL_ASCSU
AC P31889;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1996 (Rel. 33, Last annotation update)
DE FMRFamide-like neuropeptide AFl.
OS Acartis suum (pig roundworm) (Acartis lumbricoles).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascarididae;
OC Ascarididae; Acartis.
OX NCBI_TaxId=6253;
[1]
RN SEQUENCE.
RP MEDLINE=90180465; PubMed=2627377;
RX Cowden C., Stretton A.O.W., Davis R.E.;
RA "AFl, a sequenced bioactive neuropeptide isolated from the nematode
RT Acartis suum.";
RL Neuron 21:1465-1473(1989).
CC -1- FUNCTION: POTENT MODULATOR OF INHIBITORY MOTONEURONS. REDUCES THE
CC INPUT RESISTANCE AND BLOCKS SLOW OSCILLATORY POTENTIALS IN THESE
CC CELLS.
CC -1- TISSUE SPECIFICITY: FOUND IN THE NERVE CORDS AND A VARIETY OF
CC GANGLIA PARTICULARLY IN THE ANTERIOR REGIONS.
CC -1- SIMILARITY: BELONGS TO THE FMRF (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
KM Neuropeptide; Amidation.
FT MOD_RES 7 7 AMIDATION.
SQ SEQUENCE 7 AA; 953 MW; 69D40059CB144350 CRC64;

Query Match 28.3%; Score 13; DB 1; Length 7;
Best Local Similarity 16.7%; Pred. No. 1.1e+05;
Matches 1; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 3 KSQIVK 8
|:::|
Db 1 KNEFIR 6

RESULT 9
MALE_KLEPN STANDARD; PRT; 10 AA.
ID MALE_KLEPN
AC Q05364;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Maltose-binding periplasmic protein (Maltodextrin-binding protein)
DE (MBP) (Fragment).
GN MALE.
OS Klebsiella pneumoniae.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Klebsiella.
OX NCBI_TaxId=573;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=1033-5P14 / KAY2026;
RX MEDLINE=93211295; PubMed=8459773;
RA Bachellier S., Perrin D., Hofnung M., Gibson E.;
RT "Bacterial interspersed mosaic elements (BIMs) are present in the
RT genome of Klebsiella.";
RL Mol. Microbiol. 7:537-544(1993).
CC -1- FUNCTION: MALE IS INVOLVED IN THE HIGH-AFFINITY MALTOSE MEMBRANE
CC TRANSPORT SYSTEM. INITIAL RECEPTOR FOR THE ACTIVE TRANSPORT OF AND

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CC CHROMOTAXIS TOWARD MALTOLOGOSACCHARIDES.
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL EXTRACELLULAR SOLUTE-BINDING
CC PROTEIN FAMILY 1.
-----
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-----
DR EMBL; X68329; CAA8406.1; -.
DR InterPro; IPR000567; SBP_bac.1.
DR PROSITE; PS01037; SBP_BACTERIAL.1; PARTIAL.
KM Transport; Sugar transport; Periplasmic.
FT NON_TER 1
SQ SEQUENCE 10 AA; 1159 MW; 8FD8DC4415A6DDA CRC64;

Query Match 28.3%; Score 13; DB 1; Length 10;
Best Local Similarity 33.3%; Pred. No. 7.5e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 3 KSQLVK 8
DB 5 QSRITK 10

RESULT 10
ID RS10 SERMA STANDARD; PRT; 9 AA.
AC O68936;
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S10 (Fragment).
GN RpsJ.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A.
RA Noorant S.M., Lindahl L., Zengel J.M.;
RL Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Involved in the binding of tRNA to the ribosomes (By
CC similarity).
CC -1- SIMILARITY: BELONGS TO THE S10P FAMILY OF RIBOSOMAL PROTEINS.
-----
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-----
DR EMBL; AF058451; AAC14294.1; -.
DR InterPro; IPR001848; Ribosomal_S10.
DR PROSITE; PS00361; RIBOSOMAL_S10; PARTIAL.
KM Ribosomal protein.
FT NON_TER 9
SQ SEQUENCE 9 AA; 1214 MW; DE3944004416D456 CRC64;

Query Match 26.1%; Score 12; DB 1; Length 9;
Best Local Similarity 14.3%; Pred. No. 1.1e+05;
Matches 1; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKSQLVK 8
DB 1 MONQIR 7

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RESULT 11
ID TKNB_RANRI STANDARD; PRT; 10 AA.
AC P29135;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Neurokinin A.
OS Rana ridibunda (Laughing frog) (Marsh frog).
CC Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
OX NCBI_TaxID=8406;
RN [1]
RP SEQUENCE.
RC TISSUE=skin;
RX MEDLINE=93075037; PubMed=1332683;
RA Wang Y., Badgery-Parker T., Lovas S., Chartrel N., Vaudry H.,
RA Burcher E., Conlon J.M.;
RT "Primary structure and receptor-binding properties of a neurokinin A-
RT related peptide from frog gut."
RL Biochem J 287:827-832(1992).
CC -1- FUNCTION: TACHYKININS ARE ACTIVE PEPTIDES WHICH EXCITE NEURONS,
CC EVOKE BEHAVIORAL RESPONSES, ARE POTENT VASODILATORS AND
CC SECRETAGOGUES, AND CONTRACT (DIRECTLY OR INDIRECTLY) MANY SMOOTH
CC MUSCLES.
CC -1- SIMILARITY: BELONGS TO THE TACHYKININ FAMILY.
-----
DR InterPro; IPR002040; Tachykinin.
DR PROSITE; PS00267; TACHYKININ.1.
KM Tachykinin; Neuropeptide; Amidation; Amphibian skin.
FT MOD_RES 10
FT AMIDATION.
SQ SEQUENCE 10 AA; 1160 MW; 526B407059D5BAA7 CRC64;

Query Match 26.1%; Score 12; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLKLS 4
DB 2 KLKLS 5

RESULT 12
ID LPMs_STAEP STANDARD; PRT; 8 AA.
AC P23211;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 01-MAR-1992 (Rel. 21, Last annotation update)
DE Probable masr leader peptide.
OS Staphylococcus epidermidis.
OC Plasmid pUL5050.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=968;
RX MEDLINE=91041730; PubMed=2231255;
RA Ross J.I., Bady E.A., Cove J.H., Cunliffe W.J., Baumberg S.,
RA Woonton J.C.;
RT "Inducible erythromycin resistance in staphylococci is encoded by a
RT member of the ATP-binding transport super-gene family."
RL Mol. Microbiol. 4:1207-1214(1990).
CC -1- FUNCTION: MAY REGULATE EXPRESSION OF THE ERYTHROMYCIN RESISTANCE
CC PROTEIN.
-----
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CC EMBL; X52085; CAA36303.1; -
 DR PIR; S1157; LFSAME.
 KW Leader peptide; Plasmid.
 SQ SEQUENCE 8 AA; 937 MW; FA37340685BDC1A6 CRC64;

Query Match 23.9%; Score 11; DB 1; Length 8;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KX 3
 :||
 Db 6 RLX 8

RESULT 13

LPCL STAU STANDARD; PRT; 9 AA.

AC P36884;
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Chloraemphenicol resistance leader peptide.
 OS Staphylococcus aureus, and
 OS Streptococcus agalactiae.
 OG Plasmid pSCS6, Plasmid PUB112, and Plasmid pIP501.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=1280, 1311;

RP SEQUENCE FROM N.A.
 RC SPECIES=S.aureus; STRAIN=436; PLASMID=pSCS7;
 RX MEDLINE=92027652; PubMed=1929326;
 RA Schwarz S., Cardoso M.;
 RT "Nucleotide sequence and phylogeny of a chloramphenicol
 acetyltransferase encoded by the plasmid pSCS7 from Staphylococcus
 aureus."
 RL Antimicrob. Agents Chemother. 35:1551-1556(1991).

RP SEQUENCE FROM N.A.
 RC SPECIES=S.aureus; PLASMID=pSCS6;
 RX MEDLINE=92388047; PubMed=1517170;
 RA Cardoso M., Schwarz S.;
 RT "Nucleotide sequence and structural relationships of a
 chloramphenicol acetyltransferase encoded by the plasmid pSCS6 from
 Staphylococcus aureus."
 RL J. Appl. Bacteriol. 72:289-293(1992).

RP SEQUENCE FROM N.A.
 RC SPECIES=S.aureus; PLASMID=pUB112;
 RX MEDLINE=86081739; PubMed=3865770;
 RA Brueckner R., Matzura H.;
 RT "Regulation of the inducible chloramphenicol acetyltransferase gene
 of the Staphylococcus aureus plasmid pUB112."
 RL EMBO J. 4:2295-2300(1985).

RP SEQUENCE FROM N.A.
 RC SPECIES=S.agalactiae; PLASMID=pIP501;
 RX MEDLINE=93096867; PubMed=1461942;
 RA Trier-Cuot P., de Cespedes G., Horand T.;
 RT "Nucleotide sequence of the chloramphenicol resistance determinant of
 the streptococcal plasmid pIP501."
 RL Plasmid 28:272-276(1992).

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CC EMBL; M58515; AAA26612.1; -

DR EMBL; M58516; AAA16528.1; -
 DR EMBL; X02872; CAA26630.1; -
 DR EMBL; X60827; CAA33217.1; -
 DR EMBL; X65462; CAA46454.1; -
 DR PIR; B24362; B24362.
 KW Leader peptide; Antibiotic resistance; Plasmid.
 SQ SEQUENCE 9 AA; 1074 MW; 5D9CAB5AAB05B33 CRC64;

Query Match 23.9%; Score 11; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KSQ 5
 :||
 Db 3 KSE 5

RESULT 14

ULAK MOUSE STANDARD; PRT; 9 AA.

AC P99031;
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Unknown protein from 2D-page of liver tissue (Spot 2D-0014LD)
 DE (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;

RP SEQUENCE.
 RC TISSUE=Liver;
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
 RA Couthorne M.;
 RL Submitted (Aug-1998) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL, THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 6.0, ITS MW IS: 12.5 kDa.
 DR SWISS-2DPAGE; P99031; MOUSE.

FT NON_TER
 SQ SEQUENCE 9 AA; 1106 MW; E1E842C3240B145A CRC64;
 Query Match 23.9%; Score 11; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.1e+05;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 KRX 10
 :||
 Db 4 ERK 6

RESULT 15

RCA PINPS STANDARD; PRT; 10 AA.

AC P81084;
 DT 15-JUN-1998 (Rel. 36, Last sequence update)
 DT 15-JUN-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Probable ribulose biphosphate carboxylase/oxygenase activase (Rubisco
 DE activase) (RA) (Water stress responsive protein 4) (Fragment).
 OS Pinus pinaster (Maritime pine).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.

NCBI_TaxID=71647;

RP SEQUENCE.

RC TISSUE=Needle;

RX MEDLINE=98418576; PubMed=9747804;
 RA Costa P., Bahman N., Frigerio J.-M., Kremer A., Plomion C.;
 RT "Water-deficit-responsive proteins in maritime pine."
 RL Plant Mol. Biol. 38:587-596(1998).

CC [2]

RP SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RA Costa P., Pionneau C., Bauw G., Dubois C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
proteins";
RL Electrophoresis 20:1098-1108 (1999).
CC -1- FUNCTION: ACTIVATION OF RUBISCO (RUBULOSE-1,5-BISPHOSPHATE
CARBOXYLASE/OXYGENASE; EC 4.1.1.39) INVOLVES THE ATP-DEPENDENT
CC CARBOXYLATION OF THE EPSILON-AMINO GROUP OF LYSINE LEADING TO A
CC CARBAMATE STRUCTURE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
CC -1- INDUCTION: BY WATER STRESS.
CC -1- SIMILARITY: BELONGS TO THE RUBISCO ACTIVASE FAMILY.
KW Chloroplast; ATP-binding.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA, 1171 MW; C0A506D2C72B1E86 CRC64;

Query Match 23.9%; Score 11; DB 1; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.8e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 5 QLVKRX 10
: || |
Db 5 ELVPAK 10

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(without alignments)
73.588 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KLSQVLKRRK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 1224

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvlnus:*
16: sp_bacteria:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Length	DB ID	Description
1	18	39.1	8	12	Q84273 human papill
2	17	37.0	9	7	078226 mus musculu
3	17	37.0	10	10	Q94119 zea mays (m
4	16	34.8	7	4	Q15897 homo sapien
5	16	34.8	7	12	Q9YVE3 human adeno
6	16	34.8	7	12	Q9YIR0 human adeno
7	16	34.8	7	12	Q9YIC9 human adeno
8	16	34.8	8	12	Q83977 human adeno
9	16	34.8	8	13	Q83977 Influenzavi
10	15	32.6	8	2	Q92E29 oncorhynchu
11	15	32.6	8	2	Q92E29 buchneera ap
12	15	32.6	8	2	Q56429 thermus the
13	15	32.6	8	12	Q47273 escherichia
14	15	32.6	9	4	Q84271 human papil
15	15	32.6	9	4	Q16276 homo sapien
16	15	32.6	9	6	Q9YU0 monodelphis
			9	12	Q71067 canine diet

17	15	32.6	9	12	Q71068	Q71068 canine diet
18	15	32.6	10	2	Q9F5W1	Q9F5W1 vibrio chol
19	14	30.4	8	2	P72279	P72279 rhodococcus
20	14	30.4	8	8	Q34909	Q34909 locusta mig
21	14	30.4	9	7	Q78225	Q78225 mus musculu
22	14	30.4	10	2	Q921B1	Q921B1 clostridium
23	14	30.4	10	2	Q9JNC9	Q9JNC9 streptococ
24	14	30.4	10	2	Q47651	Q47651 escherichia
25	14	30.4	10	8	P82136	P82136 spinacia ol
26	14	30.4	10	13	Q9PRU1	Q9PRU1 cynops pyr
27	14	30.4	10	15	Q8UT83	Q8UT83 human immun
28	13	28.3	9	4	Q15891	Q15891 homo sapien
29	13	28.3	9	4	Q9UE26	Q9UE26 homo sapien
30	13	28.3	9	5	Q8MS88	Q8MS88 antioxiidari
31	13	28.3	9	5	Q95GN1	Q95GN1 pelargonium
32	13	28.3	10	1	Q9UMW5	Q9UMW5 sulfolobus
33	13	28.3	10	2	Q9S3J6	Q9S3J6 escherichia
34	13	28.3	10	3	Q9HDS1	Q9HDS1 aspergillus
35	13	28.3	10	4	Q9H121	Q9H121 homo sapien
36	13	28.3	10	9	Q38217	Q38217 lactococcus
37	12	26.1	7	8	P92372	P92372 haynaldia v
38	12	26.1	7	8	P92403	P92403 lophopyrum
39	12	26.1	7	8	P92425	P92425 pseudoeogn
40	12	26.1	7	8	P92387	P92387 henaridia p
41	12	26.1	7	8	P92427	P92427 peridictyon
42	12	26.1	7	8	P92390	P92390 heteranthe
43	12	26.1	7	8	P92226	P92226 crithopsis
44	12	26.1	7	8	P92214	P92214 amblyopyrum
45	12	26.1	7	8	P92430	P92430 aegilops ta

ALIGNMENTS

RESULT 1
Q84273 PRELIMINARY; PRT; 8 AA.
ID Q84273
AC Q84273;
DT 01-NOV-1996 (T-REMBLrel. 01, Created)
DT 01-NOV-1996 (T-REMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (T-REMBLrel. 08, Last annotation update)
DE L1 protein (Fragment).
OS Human papillomavirus type 25.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10609;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=8089511; PubMed=282651;
RA Krubke J., Kraus J., Dellus H., Chow L., Broker T.R., Ifner T., Pfister H.,
RT "Genetic Relationship among human papillomaviruses associated with
RT benign and malignant tumors of patients with epidermodyplasia
RT veruiciformis.",
RL J. Gen. Virol. 68:3091-3103(1987).
DR EMBL; D00205; BAA00144.1; -.
FT NON TER 1 1
SQ SEQUENCE 8 AA; 999 MW; 7F43240324033058 CRC64;
Query Match 39.1%; Score 18; DB 12; Length 8;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 7 VKRK 10
Db 2 IKRK 5
RESULT 2
ID Q78226 PRELIMINARY; PRT; 9 AA.
AC Q78226;
DT 01-NOV-1998 (T-REMBLrel. 08, Created)

DT 01-NOV-1998 (TReMBLrel. 08, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE Lymphocyte antigen (Fragment).
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CRO437; TISSUE=KIDNEY;
 RX MEDLINE=88084418; PubMed=3592165;
 RA Golubie M., Budinir O., Schoepfer R., Kaahara M., Mayer W.E.,
 RA Figueroa F., Klein J.;
 RT "Nucleotide sequence analysis of class II genes borne by mouse L
 RT chromosomes."
 RL Genet. Res. 50:137-146(1987).
 DR EMBL; L38590; AAA57294.1; -.
 FT NON_TER 1 1
 FT NON_TER 9 9
 SQ SEQUENCE 9 AA; 1176 MW; 86CB1412C729C33A CRC64;

Query Match 37.0%; Score 17; DB 7; Length 9;
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 6 VKRR 10
 DB 5 LVRR 9

RESULT 3
 ID 094119 PRELIMINARY; PRT; 10 AA.
 AC 094119;
 DT 01-DEC-2001 (TReMBLrel. 19, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE Anthocyanin regulator R-sc protein (Fragment).
 OS Zea mays (Maize).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 CC Panicoidae; Andropogoneae; Zea.
 CX NCBI_TaxID=4577;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prociissi A., Piazza P., Tonelli C.;
 RT "A maize r1 gene is regulated post-transcriptionally by differential
 RT splicing of its leader."
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY029766; AAK61356.1; -.
 FT NON_TER 10 10
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1074 MW; 9CC9E4DDDD736C5 CRC64;

Query Match 37.0%; Score 17; DB 10; Length 10;
 Best Local Similarity 60.0%; Pred. No. 9.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LKSQL 6
 DB 1 MRSOL 5

RESULT 4
 ID 015897 PRELIMINARY; PRT; 7 AA.
 AC 015897;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE (Clone XPEA11A) (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

CX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
 RA Coolbaugh M.L., Chinnault C.A., Baldini A., Lindsay E.A., Zhao Z.-Y.,
 RA Caskey C.T.H.;
 RT "Isolation of chromosome-specific genes by reciprocal probing of
 RT arrayed cDNAs and cosmid libraries."
 RL Hum. Mol. Genet. 0:0-0(1995).
 DR EMBL; L32077; AAA73887.1; -.
 FT NON_TER 1 1
 FT NON_TER 7 7
 SQ SEQUENCE 7 AA; 814 MW; 672B1DD3372046B0 CRC64;

Query Match 34.8%; Score 16; DB 4; Length 7;
 Best Local Similarity 60.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LKSQL 6
 DB 3 LKAEI 7

RESULT 5
 ID 09YVE3 PRELIMINARY; PRT; 7 AA.
 AC 09YVE3;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, last annotation update)
 DE PVI core protein (Fragment).
 GN PVI.
 OS Human adenovirus type 7.
 CC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 CX NCBI_TaxID=10519;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GOMEN;
 RX MEDLINE=99175282; PubMed=10074533;
 RA Crawford-Mikeza L.K., Nang R.N., Schurr D.P.;
 RT "Strain variation in adenovirus serotypes 4 and 7a causing acute
 RT respiratory disease."
 RL J. Clin. Microbiol. 37:1107-1112(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=GOMEN;
 RA Crawford-Mikeza L.K.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF065065; AAD03662.1; -.
 FT NON_TER 1 1
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 34.8%; Score 16; DB 12; Length 7;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 7 VKRR 10
 DB 1 VKRR 4

RESULT 6
 ID 09YIRO PRELIMINARY; PRT; 7 AA.
 AC 09YIRO;
 DT 01-MAY-1999 (TReMBLrel. 10, Created)
 DT 01-MAY-1999 (TReMBLrel. 10, last sequence update)
 DT 01-OCT-2001 (TReMBLrel. 18, last annotation update)
 DE PVI core protein (Fragment).
 GN PVI.
 OS Human adenovirus type 7a.
 CC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.

OX NCBI_TaxID=85755;
 RN [1]
 RT SEQUENCE FROM N.A.
 RC STRAIN=KN 796-0620, S-1058, AND CL 68578;
 RA Crawford-Mikeza L.K., Nang R.N., Schurr D.P.;
 RT "Molecular surveillance of strain variation in adenoviruses causing
 acute respiratory disease, AV 4 and AV 7a."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF065068; AAD03664.1; -.
 DR EMBL; AF065066; AAD03664.1; -.
 DR EMBL; AF065067; AAD03666.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 34.8%; Score 16; DB 12; Length 7;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VKRK 10
 DB 1 VKRR 4

RESULT 7
 Q9YIQ9 PRELIMINARY; PRT; 7 AA.

AC Q9YIQ9;
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-OCT-2001 (T-EMBLrel. 18, Last annotation update)
 DE PVI core protein (Fragment).
 GN PVI.
 OS Human adenovirus type 4.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 OX NCBI_TaxID=28280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2-G 95-873, RI-67, AND 55142;
 RA Crawford-Mikeza L.K., Nang R.N., Schurr D.P.;
 RT "Molecular surveillance of strain variation in adenoviruses causing
 acute respiratory disease, AV 4 and AV 7a."
 RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF065064; AAD03659.1; -.
 DR EMBL; AF065062; AAD03653.1; -.
 DR EMBL; AF065063; AAD03656.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 7 AA; 980 MW; 7B5EA414140322A0 CRC64;

Query Match 34.8%; Score 16; DB 12; Length 7;
 Best Local Similarity 75.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VKRK 10
 DB 1 VKRR 4

RESULT 8
 Q83977 PRELIMINARY; PRT; 8 AA.

AC Q83977;
 DT 01-NOV-1996 (T-EMBLrel. 01, Created)
 DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last annotation update)
 DE Influenza A/udorn/72 (H3n2), nucleoprotein (Seg 5), 5' cDNA
 (Fragment).
 OS Influenzavirus A.
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenza A viruses.
 OX NCBI_TaxID=11320;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=83112211; PubMed=6296449;

RA Lin B.-C., Lai C.-J.;
 RT "The influenza virus nucleoprotein synthesized from cloned dna in a
 simian virus 40 vector is detected in the nucleus."
 RL J. Virol. 45:434-438(1983).
 DR EMBL; J02170; AAA43468.1; -.
 KW Nucleocapsid.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 878 MW; ED0321A86C5BDD6 CRC64;

Query Match 34.8%; Score 16; DB 13; Length 8;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 KXSOLVK 9
 DB 1 MASQTKR 8

RESULT 9
 P87488 PRELIMINARY; PRT; 8 AA.

AC P87488;
 DT 01-MAY-1997 (T-EMBLrel. 03, Created)
 DT 01-MAY-1997 (T-EMBLrel. 03, Last sequence update)
 DE Growth hormone 2 (Fragment).
 GN GH-2-A OR GH-2-B.
 OS Oncorhynchus kisutch (Coho salmon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8019;
 RN [1]
 RP SEQUENCE OF 41-48 FROM N.A.
 RX MEDLINE=94173883; PubMed=8127856;
 RA Forbes S.H., Knudsen K.L., North T.W., Allendorf F.W.;
 RT "One of two growth hormone genes in coho salmon is sex-linked."
 RL Proc. Natl. Acad. Sci. U.S.A. 91:1628-1631(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Forbes S.H., Knudsen K.L., North T.W., Allendorf F.W.;
 RL Proc. Natl. Acad. Sci. U.S.A. 91:0-0(0).
 DR EMBL; U04930; AAD13472.1; -.
 DR EMBL; U04931; AAD13476.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 8 AA; 902 MW; 92233732D5A5B326 CRC64;

Query Match 34.8%; Score 16; DB 13; Length 8;
 Best Local Similarity 50.0%; Pred. No. 6.7e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KXSOLVK 8
 DB 2 KSSVTK 7

RESULT 10
 Q9ZE29 PRELIMINARY; PRT; 8 AA.

AC Q9ZE29;
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last annotation update)
 DE 2-isopropylmalate synthase (BC 4.1.3.12) (Fragment).
 GN IEUA.
 OS Buchnera aphidicola.
 OC Plasmid pBRc1.
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=9;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99028904; PubMed=9812361;

RA Silva F.J., Van Ham R.C.H.J., Sabater B., Latorre A.;
RT "Structure and evolution of the leucine plasmids carried by the
RT endosymbiont (Buchnera aphidicola) from aphids of the family
RT Aphididae.";
RL FEWS Microbiol. Lett. 168:43-49 (1998).
DR EMBL; AJ006874; CAA07290.1; -.
KW Lyase; Plasmid.
FT NON TER
SQ SEQUENCE 8 AA; 917 MW; FE205042D6C5B446 CRC64;

Query Match 32.6%; Score 15; DB 2; Length 8;
Best Local Similarity 33.3%; Pred. No. 6.7e+05;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 LKSQLV 7
DB 1 MNSQVI 6

RESULT 11
Q56429 PRELIMINARY; PRT; 8 AA.
ID O56429
AC O56429;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE GAPDH (Fragment).
OS Thermus thermophilus.
OC Bacteria; Thermus/Deinococcus group; Deinococci; Thermales;
OC Thermaceae; Thermus.
OX NCBI_TaxID=274;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HB-8;
RX MEDLINE=89025722; PubMed=3052437;
RA Bowen D., Littlechild J.A., Fothergill J.E., Watson H.C., Hall L.;
RT "Nucleotide sequence of the phosphoglycerate kinase gene from the
RT extreme thermophile, Thermus thermophilus.";
RL Biochem. J. 254:509-517 (1988).
DR EMBL; X12464; CAA31005.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 885 MW; 33C87333732C72B CRC64;

Query Match 32.6%; Score 15; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 QLVKRX 10
DB 1 ELVLKK 6

RESULT 12
Q47273 PRELIMINARY; PRT; 8 AA.
ID Q47273
AC Q47273;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Orlf33, orf151, orf56, orf96, rus, orf45, orf127, and nmpc
DE genes.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K-12;
RX MEDLINE=96196428; PubMed=8648624;
RA Mahdi A.A., Sharples G.J., Mandal T.N., Lloyd R.G.;
RT "Holiday Junction Resolvases encoded by homologous rusa genes in
RT Escherichia coli K-12 and phage 32.";
RL J. Mol. Biol. 257:561-573 (1996).

DR EMBL; X92587; CAA63323.1; -.
SQ SEQUENCE 8 AA; 935 MW; FD4041A05B05B336 CRC64;

Query Match 32.6%; Score 15; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 6.7e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 2 LKSQL 6
DB 1 MKSEI 5

RESULT 13
Q84271 PRELIMINARY; PRT; 8 AA.
ID Q84271
AC Q84271;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE L1 protein (Fragment).
OS Human papillomavirus type 19.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Papillomavirus.
OX NCBI_TaxID=10608;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88089511; PubMed=282651;
RA Krubke J., Kraus J., Dellus H., Chow L., Broker T.R., Iftner T.,
RA Pfister H.;
RT "Genetic relationship among human papillomaviruses associated with
RT benign and malignant tumors of patients with epidermodysplasia
RT verruciformis.";
RL J. Gen. Virol. 68:3091-3103 (1987).
DR EMBL; D00204; BAA00142.1; -.
FT NON TER
SQ SEQUENCE 8 AA; 987 MW; 7F432403240321A8 CRC64;

Query Match 32.6%; Score 15; DB 12; Length 8;
Best Local Similarity 100.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 KRX 10
DB 3 KRX 5

RESULT 14
Q16276 PRELIMINARY; PRT; 9 AA.
ID Q16276
AC Q16276;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE Neurofibromatosis type 2 (Fragment).
GN NF2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95038750; PubMed=7951241;
RA Arai E., Ikeuchi T., Nakamura Y.;
RT "Characterization of the translocation breakpoint on chromosome
RT 22q12.2 in a patient with neurofibromatosis type 2 (NF2).";
RL Hum. Mol. Genet. 3:937-939 (1994).
DR EMBL; S75841; AAD14190.2; -.
FT NON TER
SQ SEQUENCE 9 AA; 1044 MW; 1E4CBD337232404 CRC64;

Query Match 32.6%; Score 15; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KLKS 4
|||:
Db 4 KLKA 7

RESULT 15

Q9TUY0 PRELIMINARY; PRT; 9 AA.
ID Q9TUY0
AC Q9TUY0;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Acetyl-CoA acetyltransferase 2 (Fragment).
GN ACAT2.
OS Monodelphis domestica (Short-tailed grey opossum).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Monodelphis.
OX NCBI_TaxID=13616;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99282512; PubMed=10353914;
RA Spinant S., O'hugin C., Toyosawa S., Michalova V., Klein J.;
RT "Origin of gene overlap. The case of tcpl and acat2."
RL Genetics 152:743-754(1999).
DR EMBL; AF143498; AAD34974.1; -.
KW Transferase.
FT NON TER 1 1
SQ SEQUENCE 9 AA; 1006 MW; 119F0322CEB69DD0 CRC64;

Query Match 32.6%; Score 15; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 6.7e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 VKRK 10
|||:
Db 6 VKRE 9

Search completed: February 8, 2003, 11:04:01
Job time : 30 secs

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OM protein - protein search, using sw model

Run on: February 8, 2003, 10:59:12 ; Search time 34 Seconds
(without alignments)
39.191 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KLSQQLVKKR 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 908470 seqs, 133250620 residues
Total number of hits satisfying chosen parameters: 174064

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: /SID2/gcgdata/geneseq/geneseq-emb1/AA1980.DAT*
2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT*
3: /SID2/gcgdata/geneseq/geneseq-emb1/AA1982.DAT*
4: /SID2/gcgdata/geneseq/geneseq-emb1/AA1983.DAT*
5: /SID2/gcgdata/geneseq/geneseq-emb1/AA1984.DAT*
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7: /SID2/gcgdata/geneseq/geneseq-emb1/AA1986.DAT*
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9: /SID2/gcgdata/geneseq/geneseq-emb1/AA1988.DAT*
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12: /SID2/gcgdata/geneseq/geneseq-emb1/AA1991.DAT*
13: /SID2/gcgdata/geneseq/geneseq-emb1/AA1992.DAT*
14: /SID2/gcgdata/geneseq/geneseq-emb1/AA1993.DAT*
15: /SID2/gcgdata/geneseq/geneseq-emb1/AA1994.DAT*
16: /SID2/gcgdata/geneseq/geneseq-emb1/AA1995.DAT*
17: /SID2/gcgdata/geneseq/geneseq-emb1/AA1996.DAT*
18: /SID2/gcgdata/geneseq/geneseq-emb1/AA1997.DAT*
19: /SID2/gcgdata/geneseq/geneseq-emb1/AA1998.DAT*
20: /SID2/gcgdata/geneseq/geneseq-emb1/AA1999.DAT*
21: /SID2/gcgdata/geneseq/geneseq-emb1/AA2000.DAT*
22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	46	100.0	10	23	ABG60827
2	43	93.5	10	14	AAK46551
3	43	93.5	10	18	AAW39164
4	39	84.8	10	18	AAW39168
5	38	82.6	9	14	AAK46550
6	38	82.6	9	23	ABG60850
7	38	82.6	10	23	AAU11442
8	31	67.4	10	18	AAW39167
9	25	54.3	9	17	AAK9730
10	25	54.3	9	17	AAK9725

11	24	52.2	10	22	AA95218	Human complement
12	23	50.0	9	23	ABG35074	Hodgkin's disease
13	23	50.0	10	16	AAK90268	Ion-channel formin
14	23	50.0	10	20	AA10768	Peptide used to ma
15	23	50.0	10	23	AAK22481	Biologically activ
16	22	47.8	10	16	AAK80709	CXC Interferin fam
17	22	47.8	10	20	AAW94809	Peptide tested for
18	22	47.8	10	21	AAK23426	Peptide #50 tested
19	22	47.8	10	22	AAK57900	Human complement
20	22	47.8	10	22	AAK87030	Saccharomyces cere
21	22	47.8	10	22	AAK87032	Saccharomyces cere
22	22	47.8	10	23	AAK23535	Peptide #2 used to
23	22	45.7	8	20	ABP14702	HIV A03 super moti
24	21	45.7	8	22	ABP15078	HIV A03 super moti
25	21	45.7	8	22	ABP21124	HIV A03 motif pol
26	21	45.7	8	22	ABP22190	HIV A03 motif vpr
27	21	45.7	8	22	ABP23150	HIV A11 motif pol
28	21	45.7	8	22	ABP23981	HIV A11 motif vpr
29	21	45.7	8	23	ABK74553	DNA repair protein
30	21	45.7	9	20	AAV53311	Bcr-Abl epitope (a
31	21	45.7	9	20	AAV53345	Bcr-Abl epitope (a
32	21	45.7	9	20	AAV40133	Amino acid sequenc
33	21	45.7	9	20	AAV40167	Amino acid sequenc
34	21	45.7	9	20	AAV26683	BCR-ABL-derived 11
35	21	45.7	9	20	AAV26649	BCR-ABL-derived 11
36	21	45.7	9	20	AAW82590	Human fibronectin
37	21	45.7	9	22	ABP13500	HIV A02 super moti
38	21	45.7	9	22	ABP16068	HIV A24 super moti
39	21	45.7	9	22	ABP19061	HIV B62 super moti
40	21	45.7	9	22	ABP22195	HIV A03 motif vpr
41	21	45.7	9	22	AAU06877	Human MHC molecule
42	21	45.7	9	22	AAU06945	Human MHC molecule
43	21	45.7	9	22	AAU07007	Human MHC molecule
44	21	45.7	10	15	AAK46274	Antigenic fragment
45	21	45.7	10	16	AAK80710	CXC Interferin fam

ALIGNMENTS

RESULT 1					
ID	ABG60827	standard; Peptide; 10 AA.			
XX	ABG60827				
AC	ABG60827				
XX					
DT	13-AUG-2002	(first entry)			
XX					
DE	Hyaluronan (HA) binding peptide #10.				
XX					
KW	Tissue disorder; response-to-injury process; cell proliferating;				
KW	hyaluronic acid; HA; receptor for hyaluronan-mediated motility;				
KW	Rheum; inflammatory neurological disorder; Parkinson's disease;				
KW	Alzheimer's disease; arthritis; multiple sclerosis; gastritis; nephritis;				
KW	inflammatory dermatosis; psoriasis; inflammatory bowel disease;				
KW	stenosis; restenosis; cancer; kidney fibrosis; inflammatory lung disease;				
KW	emphysema; asthma; cystic fibrosis; obesity; obesity related disease;				
KW	lupus; cardiovascular disease; atherosclerosis; wound; scar; diabetes;				
KW	tissue transplantation; stroke; inflammatory response; fibrotic response;				
KW	medical implant; Acquired immunodeficiency syndrome; AIDS; hepatitis;				
KW	myocardial fibrosis; hepatic fibrosis; chronic cystitis; acute mastitis;				
KW	septic shock; thyroiditis; retinopathy.				
XX					
OS	Synthetic.				
XX					
PN	WO200228415-A1.				
XX					
PD	11-APR-2002.				
XX					
PF	05-OCT-2000; 2000WO-IB01534.				
XX					
PR	05-OCT-2000; 2000WO-IB01534.				
XX					

PA (TRAN-) TRANSITION THERAPEUTICS & DIAGNOSTICS IN.
 XX
 XX
 PI Turley EA, Cruz TF;
 XX
 XX
 DR WPI; 2002-435298/46.
 XX
 XX
 PT Treating tissue disorder associated with response-to-injury process or
 PT proliferating cells in mammals, e.g. fibrosis, inflammation, by
 PT administering a compound that alters activity of transition molecules
 PT within a cell
 XX
 PS Example 31; Page 115; 215pp; English.
 XX
 CC The invention describes a method of treating a tissue disorder associated
 CC with response-to-injury process or proliferating cells in a patient,
 CC comprising administering a polypeptide (I) which binds hyaluronic acid
 CC (HA), an antibody which binds one of domains D1-D5 of Receptor for
 CC hyaluronan-mediated motility (RHAMM), a polypeptide fragment encoding
 CC any of D1-D5 of RHAMM, or a vector which expresses antisense RHAMM,
 CC antibodies or a polypeptide fragment. The method is useful for treating a
 CC patient with an inflammatory neurological disorder such as Parkinson's
 CC disease, Alzheimer's disease, arthritis including rheumatoid arthritis,
 CC osteoarthritis, multiple sclerosis, inflammatory dermatosis (psoriasis),
 CC inflammatory bowel disease, stenosis or restenosis, cancer, kidney
 CC fibrosis, inflammatory lung disease (e.g. emphysema, asthma, cystic
 CC fibrosis), obesity or obesity related diseases, lupus, cardiovascular
 CC disease (e.g. atherosclerosis), and wound especially surgical excision
 CC adhesions, to prevent scar and also for treating or preventing diabetes
 CC mellitus. The method is also useful for treating tissue transplantation
 CC (e.g. skin grafts), stroke, inflammatory responses or fibrotic response
 CC associated with medical implants such as hip implants, vascular wraps and
 CC catheters), inflammatory diseases such as AIDS, myocardial and hepatic
 CC fibrosis, chronic cystitis, acute mastitis, gastritis, nephritis,
 CC hepatitis, septic shock, thyroiditis, and retinopathy. This sequence
 CC represents a hyaluronan (HA) binding peptide used in the method of
 CC treating a tissue disorder described in the invention.
 CC
 XX
 SQ Sequence 10 AA;
 Query Match 100.0%; Score 46; DB 23; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.026;
 Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLSQSLVKK 10
 Db 1 KLSQSLVKK 10
 RESULT 2
 AAR46551
 ID AAR46551 standard; Protein, 10 AA.
 XX
 XX
 AC AAR46551;
 XX
 XX
 DT 05-APR-1994 (first entry)
 XX
 XX
 DE Hyaluronan receptor binding motif (claimed).
 XX
 KW Hyaluronan binding protein; HA; RHAMM; mediated motility; wound;
 KW healing; diagnosis; treatment; cell locomotion; tumour invasion;
 KW birth defects; inflammatory disorder; Alzheimer's disease; dementia;
 KW Parkinson's disease; Huntington's disease; AIDS; diabetes; auto;
 KW immune diseases; corneal dysplasia; hypertrophy; surgery; burns;
 KW strokes; multiple sclerosis; depression; schizophrenia; CNS;
 KW contraception; in vitro fertilisation; embryo development.
 XX
 XX
 FN W09321312-A.
 XX
 PD 28-OCT-1993.
 XX
 PF 13-APR-1993; 93WO-CA00158.
 XX
 PR 05-APR-1992; 92GB-0007949.
 PR

XX
 PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
 PA (UTMA-) UNIV MANITOBA.
 XX
 XX
 PI Turley EA;
 XX
 XX
 DR WPI; 1993-351722/44.
 XX
 XX
 PT DNA encoding hyaluronan receptor - used to produce proteins and
 PT antibodies for alteration of cell locomotion
 XX
 PS Claim 18; Page 57; 88pp; English.
 XX
 CC The sequence is that of a binding motif fragment of the hyaluronan
 CC receptor (HARC). HARC is down regulated in normal cells and is only
 CC expressed in situations where cell motility is desired, e.g. in
 CC wound healing, in response to growth factors and in chemotaxis by
 CC white blood cells. HA may be used for diagnosis and treatment of
 CC diseases involving cell locomotion, e.g. tumour invasion, birth
 CC defects, acute and chronic inflammatory disorders, Alzheimer's and
 CC other forms of dementia, AIDS, diabetes, autoimmune diseases, corneal
 CC dysplasias and hypertrophies, burns, surgical incisions and adhesions,
 CC strokes, multiple sclerosis, depression/schizophrenia related to
 CC neuronal growth and pain states involving nerve sprouting, also in CNS
 CC and spinal cord regeneration, contraception, in vitro fertilisation and
 CC embryo development.
 CC See also AAR46548-50 and AAR43563.
 CC
 XX
 SQ Sequence 10 AA;
 Query Match 93.5%; Score 43; DB 14; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.097;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLSQSLVKK 10
 Db 1 KLSQSLVKK 10
 RESULT 3
 AAM39164
 ID AAM39164 standard; peptide; 10 AA.
 XX
 XX
 AC AAM39164;
 XX
 XX
 DT 27-APR-1998 (first entry)
 XX
 XX
 DE Mouse RHAMM binding domain 2 consensus motif peptide.
 XX
 KW Hyaluronan receptor; receptor for hyaluronic acid mediated motility;
 KW RHAMM; glycosaminoglycan; binding domain; mouse; oncogene; treatment;
 KW growth factor; cell locomotion disorder; dementia; detection;
 KW inflammatory disorder; autoimmune disease; diagnosis; prognosis.
 XX
 XX
 OS Mus sp.
 XX
 XX
 FN W09738098-A1.
 XX
 PD 16-OCT-1997.
 XX
 PF 10-APR-1997; 97WO-CA00240.
 XX
 PR 10-APR-1996; 96GB-0007441.
 XX
 XX
 PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
 PA (UTMA-) UNIV MANITOBA.
 XX
 PI Entwistle J, Turley EA;
 XX
 XX
 DR WPI; 1997-512715/47.
 XX
 XX
 PT Isolated human receptor for hyaluronic acid mediated motility - used
 PT to develop products for treating e.g. tumours, inflammatory

PT disorders, dementia, AIDS, diabetes and auto-immune diseases
 XX Disclousure; Fig 1; 66pp; English.
 XX
 CC This peptide represents a motif found in a binding domain of mouse
 CC hyaluronan receptor corresponding to amino acid position 424-433. This
 CC receptor is also known as the receptor for hyaluronan acid mediated
 CC motility (RHAMM). Hyaluronan is a large glycosaminoglycan that is
 CC ubiquitous in the extracellular matrix and whose synthesis has been
 CC linked to cell migration, growth and transformation. It interacts with
 CC cell surfaces via specific protein receptors, e.g. RHAMM, that mediate
 CC many biological effects. The RHAMM/Hyaluronic acid interaction is
 CC involved in oncogene-and growth factor-mediated cell locomotion. The
 CC products can be used in the treatment of disorders involving cell
 CC locomotion, e.g. tumour invasion, birth defects, acute and chronic
 CC inflammatory disorders, Alzheimer's and other forms of dementia,
 CC including Parkinson's and Huntington's diseases, AIDS, diabetes,
 CC autoimmune diseases, corneal dysplasia and hypertrophies, burns, surgical
 CC incisions and adhesions, strokes and multiple sclerosis. They can also
 CC be used in e.g. CNS and spinal cord regeneration, contraception and in
 CC vitro fertilisation and embryo development. The products can also be
 CC used in detection, diagnosis and prognosis.
 CC
 XX Sequence 10 AA;
 SQ
 Query Match 93.5%; Score 43; DB 18; Length 10;
 Best Local Similarity 90.0%; Pred. No. 0.097;
 Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KLRSQLVYRK 10
 ||:|||||
 Db 1 KLRSQLVYRK 10
 RESULT 4
 AAM39168
 ID AAM39168 standard; peptide; 10 AA.
 XX
 AC AAM39168;
 XX
 DT 27-APR-1998 (first entry)
 XX
 DE Rat RHAMM binding domain 2 consensus motif peptide.
 XX
 KM Hyaluronan receptor; receptor for hyalurononic acid mediated motility;
 KM RHAMM; glycosaminoglycan; binding domain; rat; oncogene; treatment;
 KM growth factor; cell locomotion disorder; dementia; detection;
 KM inflammatory disorder; autoimmune disease; diagnosis; prognosis.
 XX
 OS Rat sp.
 XX
 PN WO9738098-A1.
 XX
 PD 16-OCT-1997.
 XX
 PF 10-APR-1997; 97WO-CA00240.
 XX
 PR 10-APR-1996; 96GB-0007441.
 XX
 PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
 PA (UYMA-) UNIV MANITOBA.
 XX
 PI Entwistle J, Turley EA;
 XX
 DR WPI; 1997-512715/47.
 XX
 PT Isolated human receptor for hyalurononic acid mediated motility - used
 PT to develop products for treating e.g. tumours, inflammatory
 PT disorders, dementia, AIDS, diabetes and auto-immune diseases
 XX
 PS Disclousure; Fig 1; 66pp; English.
 XX
 CC This peptide represents a motif found in a binding domain of rat

CC hyaluronan receptor corresponding to amino acid position 424-433. This
 CC receptor is also known as the receptor for hyalurononic acid mediated
 CC motility (RHAMM). Hyaluronan is a large glycosaminoglycan that is
 CC ubiquitous in the extracellular matrix and whose synthesis has been
 CC linked to cell migration, growth and transformation. It interacts with
 CC cell surfaces via specific protein receptors, e.g. RHAMM, that mediate
 CC many biological effects. The RHAMM/Hyaluronic acid interaction is
 CC involved in oncogene-and growth factor-mediated cell locomotion. The
 CC products can be used in the treatment of disorders involving cell
 CC locomotion, e.g. tumour invasion, birth defects, acute and chronic
 CC inflammatory disorders, Alzheimer's and other forms of dementia,
 CC including Parkinson's and Huntington's diseases, AIDS, diabetes,
 CC autoimmune diseases, corneal dysplasia and hypertrophies, burns, surgical
 CC incisions and adhesions, strokes and multiple sclerosis. They can also
 CC be used in e.g. CNS and spinal cord regeneration, contraception and in
 CC vitro fertilisation and embryo development. The products can also be
 CC used in detection, diagnosis and prognosis.
 CC
 XX Sequence 10 AA;
 SQ
 Query Match 84.8%; Score 39; DB 18; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.55;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 KLRSQLVYRK 10
 ||:|||||
 Db 1 KLRSQLVYRK 10
 RESULT 5
 AAR46550
 ID AAR46550 standard; Protein; 9 AA.
 XX
 AC AAR46550;
 XX
 DT 05-APR-1994 (first entry)
 XX
 DE Hyaluronan receptor binding motif (claimed).
 XX
 KM Hyaluronan binding protein; HA; RHAMM; mediated motility; wound;
 KM healing; diagnosis; treatment; cell locomotion; tumour invasion;
 KM birth defects; inflammatory disorder; Alzheimer's disease; dementia;
 KM Parkinson's diseases; Huntington's disease; AIDS; diabetes; auto;
 KM immune diseases; corneal dysplasia; hypertrophy; surgery; burns;
 KM strokes; multiple sclerosis; depression; schizophrenia; CNU;
 KM contraception; in vitro fertilisation; embryo development.
 XX
 PN WO9321312-A.
 XX
 PD 28-OCT-1993.
 XX
 PF 13-APR-1993; 93WO-CA00158.
 XX
 PR 09-APR-1992; 92GB-0007949.
 XX
 PA (MANI-) MANITOBA CANCER TREATMENT & RES FOUND.
 PA (UYMA-) UNIV MANITOBA.
 XX
 PI Turley EA;
 XX
 DR WPI; 1993-351722/44.
 XX
 PT DNA encoding hyaluronan receptor - used to produce proteins and
 PT antibodies for alteration of cell locomotion
 XX
 PS Claim 17; Page 57; 88pp; English.
 XX
 CC The sequence is that of a binding motif fragment of the hyaluronan
 CC receptor (HARC). HARC is down regulated in normal cells and is only
 CC expressed in situations where cell motility is desired, e.g. in
 CC wound healing, in response to growth factors and in chemotaxis by
 CC white blood cells. HA may be used for diagnosis and treatment of
 CC diseases involving cell locomotion, e.g. tumour invasion, birth

CC defects, acute and chronic inflammatory disorders, Alzheimer's and
CC other forms of dementia, AIDS, diabetes, autoimmune diseases, corneal
CC dystrophies and hypertrophies, burns, surgical incisions and adhesions,
CC strokes, multiple sclerosis, depression/schizophrenia related to
CC neuronal growth and pain states involving nerve sprouting; also in CNS
CC and spinal cord regeneration, contraception, in vitro fertilisation and
CC embryo development.
CC See also AAR46548-51 and AAR43563.
CC
CC
SQ Sequence 9 AA;
Query Match 82.6%; Score 38; DB 14; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KXKSQLVXR 9
DB 1 KXKSQLVXR 9
RESULT 6
ABG60850
ID ABG60850 standard; Peptide; 9 AA.
XX
XX ABG60850;
XX
XX
DT 13-AUG-2002 (first entry)
XX
DE Cellular response to injury associated peptide #4.
XX
XX Tissue disorder; response-to-injury process; cell proliferating;
KM hyaluronic acid; HA; receptor for hyaluronan-mediated motility;
KM RHAMM; inflammatory neurological disorder; Parkinson's disease;
KM Alzheimer's disease; arthritis; multiple sclerosis; gastritis; nephritis;
KM inflammatory dermatosis; psoriasis; inflammatory bowel disease;
KM stenosis; restenosis; cancer; kidney fibrosis; inflammatory lung disease;
KM emphysema; asthma; cystic fibrosis; obesity; obesity related disease;
KM lupus; cardiovascular disease; atherosclerosis; wound; scar; diabetes;
KM tissue transplantation; stroke; inflammatory response; fibrotic response;
KM medical implant; Acquired immunodeficiency syndrome; AIDS; hepatitis;
KM myocardial fibrosis; hepatic fibrosis; chronic cystitis; acute mastitis;
KM septic shock; thyroiditis; retinopathy.
XX
XX Homo sapiens.
XX
XX MO200228415-A1.
XX
XX 11-APR-2002.
XX
XX 05-OCT-2000; 2000MO-IB01534.
XX
XX 05-OCT-2000; 2000MO-IB01534.
XX
XX (TRAN-) TRANSITION THERAPEUTICS & DIAGNOSTICS IN.
XX
XX Turley EA, Cruz TF;
XX
XX WPI; 2002-435298/46.
XX
XX
XX Treating tissue disorder associated with response-to-injury process or
XX proliferating cells in mammals, e.g. fibrosis, inflammation, by
XX administering a compound that alters activity of transition molecules
XX within a cell
XX
XX
XX Disclosure; Page 210; 215pp; English.
XX
XX The invention describes a method of treating a tissue disorder associated
XX with response-to-injury process or proliferating cells in a patient,
XX comprising administering a polypeptide (I) which binds hyaluronic acid
XX (HA), an antibody which binds one of domains DI-D5 of Receptor for
XX hyaluronan-mediated motility (RHAMM), a polypeptide fragment encoding
XX any of DI-D5 of RHAMM, or a vector which expresses antisense RHAMM,
XX antibodies or a polypeptide fragment. The method is useful for treating a

CC patient with an inflammatory neurological disorder such as Parkinson's
CC disease, Alzheimer's disease, arthritis including rheumatoid arthritis,
CC osteoarthritis, multiple sclerosis, inflammatory dermatosis (psoriasis),
CC inflammatory bowel disease, stenosis or restenosis, cancer, kidney
CC fibrosis, inflammatory lung disease (e.g. emphysema, asthma, cystic
CC fibrosis), obesity or obesity related diseases, lupus, cardiovascular
CC disease (e.g. atherosclerosis), and wound especially surgical excision
CC adhesions, to prevent scar and also for treating or preventing diabetes
CC mellitus. The method is also useful for treating tissue transplantation
CC (e.g. skin grafts), stroke, inflammatory responses or fibrotic response
CC associated with medical implants such as hip implants, vascular wraps and
CC catheters), inflammatory diseases such as AIDS, myocardial and hepatic
CC fibrosis, chronic cystitis, acute mastitis, gastritis, nephritis,
CC hepatitis, septic shock, thyroiditis, and retinopathy. This sequence
CC represents a peptide associated with the method of treating tissue
CC disorders described in the invention.
XX
XX
SQ Sequence 9 AA;
Query Match 82.6%; Score 38; DB 23; Length 9;
Best Local Similarity 88.9%; Pred. No. 7.8e+05;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 KXKSQLVXR 9
DB 1 KXKSQLVXR 9
RESULT 7
AAU11442
ID AAU11442 standard; Peptide; 10 AA.
XX
XX AAU11442;
XX
XX 12-MAR-2002 (first entry)
XX
XX
XX Hyaluronic acid-binding peptide #4.
XX
XX
XX Hyaluronic acid binding protein; RHAMM; gene therapy;
KM receptor for HA mediated motility; immunosuppressive; cytostatic.
KM conjugate; rheumatoid arthritis; scleroderma; liver fibrosis; cancer;
XX
XX
XX Synthetic.
XX
XX
XX Key Location/Qualifiers
XX
XX Misc-difference 7 /label= Val, Asp
XX
XX
XX WO200180899-A2.
XX
XX
XX 01-NOV-2001.
XX
XX 20-APR-2001; 2001WO-CA00533.
XX
XX 20-APR-2000; 2000US-198613P.
XX
XX (CANG-) CANGENE CORP.
XX
XX
XX Wołoski BWR, Williams AM, Sereña TJ, Wiebe DJ;
XX
XX WPI; 2002-075094/10.
XX
XX
XX Protein conjugates that selectively target certain tissues and organs
XX useful for treating and preventing various diseases, comprises
XX glucose-aminoglycan-targeting domain conjugated to a therapeutic
XX protein
XX
XX
XX Claim 8; Page 109; 121pp; English.
XX
XX The invention relates to a conjugate comprising an hyaluronic acid (HA)
XX -binding protein e.g. RHAMM (receptor of HA mediated motility) or peptide
XX contiguous with, or coupled to a polypeptide conjugated to a therapeutic
XX agent, and the polynucleotides encoding them. Also included is a method

CC for preparation of the HA-binding protein by inserting a first nucleotide
 CC sequence encoding a HA-binding protein directly linked to a second
 CC nucleotide sequence encoding a therapeutic protein into a suitable
 CC vector, expressing the vector in an acceptable host, purifying conjugate
 CC molecule from host or expression medium. The composition is useful for
 CC altering in vivo the distribution of a therapeutic agent comprising
 CC administering the composition to the animal where conjugate molecule will
 CC distribute primarily in tissues and organs containing high levels of
 CC endogenous HA and for treating mammal with a disorder where a diseased
 CC tissue of the mammal contains high level of HA e.g. rheumatoid
 CC arthritis, scleroderma, liver fibrosis and cancer. Lower therapeutic
 CC dosages required also translates into lower immunogenicity of the
 CC conjugated protein as compared to the native protein. As a result,
 CC conjugates improve patient compliance and reduce direct and indirect
 CC costs associated with the drug substance and its administration.
 CC Conjugates allows for the use, where appropriate, of lower, safer,
 CC dosages as compared to the conventional dosage requirements for the
 CC unconjugated corresponding therapeutic agent. Conjugate molecules have an
 CC increased half-life and potency, resulting in prolonged circulation of
 CC the molecule, efficient distribution into the target tissues, and
 CC increased bioavailability. The present sequence represents an
 CC HA-binding peptide of the invention.

XX Sequence 10 AA;

Query Match 82.6%; Score 38; DB 23; Length 10;
 Best Local Similarity 80.0%; Pred. No. 0.85;
 Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLRSQLVYRK 10
 ||:|||||
 Db 1 KLRSQLVYRK 10

RESULT 8

AA039167 standard; peptide; 10 AA.

AC AAM39167;

XX 27-APR-1998 (first entry)

DE Human RHAMM binding domain 2 consensus motif peptide.

XX Hyaluronan receptor; receptor for hyaluronic acid mediated motility;

KM RHAMM; glycosaminoglycan; binding domain; human; oncogene; treatment;

KM growth factor; cell locomotion disorder; dementia; detection;

KM inflammatory disorder; autoimmune disease; diagnosis; prognosis.

XX Homo sapiens.

OS WO9738098-A1.

PN 16-OCT-1997.

XX 10-APR-1997; 97WO-CA00240.

XX 10-APR-1996; 96GB-0007441.

PA (MANT-) MANITOBA CANCER TREATMENT & RES FOUND.

PI (UNIT-) UNIT MANITOBA.

XX Entwistle J, Turley EA;

XX WPI; 1997-512715/47.

XX Isolated human receptor for hyaluronic acid mediated motility - used

XX to develop products for treating e.g. tumours, inflammatory

XX disorders, dementia, AIDS, diabetes and auto-immune diseases

PS Claim 7; Fig 1; 66pp; English.

CC hyaluronan receptor corresponding to amino acid position 424-433. This
 CC receptor is also known as the receptor for hyaluronic acid mediated
 CC motility (RHAMM). Hyaluronan is a large glycosaminoglycan that is
 CC ubiquitous in the extracellular matrix and whose synthesis has been
 CC linked to cell migration, growth and transformation. It interacts with
 CC cell surfaces via specific protein receptors, e.g. RHAMM, that mediate
 CC many biological effects. The RHAMM/Hyaluronic acid interaction is
 CC involved in oncogene- and growth factor-mediated cell locomotion. The
 CC products can be used in the treatment of disorders involving cell
 CC locomotion, e.g. tumour invasion, birth defects, acute and chronic
 CC inflammatory disorders, Alzheimer's and other forms of dementia,
 CC including Parkinson's and Huntington's diseases, AIDS, diabetes,
 CC autoimmune diseases, corneal dysplasia and hypertrophic scars, surgical
 CC incisions and adhesions, strokes and multiple sclerosis. They can also
 CC be used in e.g. CNS and spinal cord regeneration, contraception and in
 CC vitro fertilisation and embryo development. The products can also be
 CC used in detection, diagnosis and prognosis.

XX Sequence 10 AA;

Query Match 67.4%; Score 31; DB 18; Length 10;
 Best Local Similarity 60.0%; Pred. No. 18;
 Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 KLRSQLVYRK 10
 ||:|||||
 Db 1 KLRSQLVYRK 10

RESULT 9
 AA039730 standard; peptide; 9 AA.

AC AAR9730;

XX 28-SEP-1996 (first entry)

DE Plasmid 167-72.54G Junction C-encoded peptide.

XX Pseudorabies virus; PRV; swine parvovirus; herpesvirus; vaccine;

KM vector; gpX secretion signal; S-PRV-040.

XX Swine parvovirus.

OS US5506128-A.

XX Key Location/Qualifiers
 FT Region 1..9 /note="capsid protein C-terminal region"

PN US5506128-A.

PD 09-APR-1996.

XX 06-SEP-1985; 85US-0773430.

XX 27-JUL-1988; 88US-0225032.

XX 06-SEP-1985; 85US-0773430.

XX 27-JAN-1986; 86US-0823102.

XX 17-JUL-1986; 86US-0887140.

XX 02-SEP-1986; 86US-0902887.

XX 20-NOV-1986; 86US-0933107.

XX 27-JUL-1987; 87US-0078519.

XX 17-JUN-1993; 93US-0078873.

PA (PRUT-) PRUTCH RES & DEV PARTNERSHIP.

XX Chiang CH, Cochran MD, Macdonald RD;

XX WPI; 1996-340868/34.

XX N-PSDB; AAT31911.

XX Recombinant bovine rhinotracheitis virus expressing antigenic

XX polypeptide - useful as multivalent vaccine, esp. against

XX parainfluenza or rotavirus

```
XX Example 28; Fig 45B; 114pp; English.
PS
XX
CC Plasmid 167-72.54G contains a pseudorabies virus (PRV) gpx
CC secretion signal-swine parvovirus A capsid fusion gene as an XbaI
CC fragment in vector pSP65. The fusion gene was prep'd. in 2 segments.
CC The junction (AAT31911) between the segment 2 and the vector includes
CC a region coding for the C-terminal region (AAR9729) of the capsid
CC protein. The fusion gene was inserted into the repeat region
CC of PRV, giving recombinant virus S-PRV-040, which can be used as a
CC vaccine to protect swine against parvovirus infection.
XX
SQ Sequence 9 AA;

Query Match          54.3%; Score 25; DB 17; Length 9;
Best Local Similarity 71.4%; Pred. No. 7.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 SOLVKRX 10
   |||: ||
Db 1 SOLIPRK 7

RESULT 10
AAR9725 AAR9725 standard; Peptide; 9 AA.
XX
AC AAR9725;
XX
DT 27-SEP-1996 (first entry)
XX
DE Plasmid 244-25.3D Junction D-encoded peptide.
XX
KW Pseudorabies virus; PRV; swine parvovirus; herpesvirus; vaccine;
KW capsid; beta-galactosidase; vector; S-PRV-065.
XX
OS Swine parvovirus.
XX
PN US5506128-A.
XX
PD 09-APR-1996.
XX
PF 06-SEP-1995; 85US-0773430.
XX
PR 27-JUL-1988; 88US-0225032.
PR 06-SEP-1985; 85US-0773430.
PR 27-JAN-1986; 86US-0823102.
PR 17-JUL-1986; 86US-0887140.
PR 02-SEP-1986; 86US-0902887.
PR 20-NOV-1986; 86US-0933107.
PR 27-JUL-1987; 87US-0078519.
PR 17-JUN-1993; 93US-0078873.
XX
PA (PRUT-) PRUTECH RES & DEV PARTNERSHIP.
XX
PI Chiang CH, Cochran MD, Macdonald RD;
XX
DR WPI; 1996-340868/34.
XX
DR N-PSDB; AAT31903.
XX
PT Recombinant bovine rhinotracheitis virus expressing antigenic
PT polypeptide - useful as multivalent vaccine, esp. against
PT parainfluenza or rotavirus
XX
XX
PS Example 26; Fig 40B; 114pp; English.
XX
CC Plasmid 244-25.3D contains an E. coli beta-galactosidase-swine
CC parovirus A capsid fusion gene as an XbaI fragment in vector pSP65.
CC The sequences of the junctions between 3 segments of the fusion
CC gene and the vector are given in AAT31801, AAT31802, AAT31902 and
CC AAT31903. The peptide (AAR9725) encoded by Junction D (AAT31903)
CC comprises the C-terminal region of capsid A. The fusion gene was
CC inserted into the repeat region of PRV, giving recombinant virus
```

```
CC S-PRV-065, which can be used as a vaccine to protect swine against
CC parvovirus infection.
XX
SQ Sequence 9 AA;

Query Match          54.3%; Score 25; DB 17; Length 9;
Best Local Similarity 71.4%; Pred. No. 7.8e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 SOLVKRX 10
   |||: ||
Db 1 SOLIPRK 7

RESULT 11
AAG95218
ID AAG95218 standard; Peptide; 10 AA.
XX
AC AAG95218;
XX
DT 18-SEP-2001 (first entry)
XX
DE Human complementary peptide, SEQ ID NO: 1412.
XX
KW Human; complementary peptide; ligand; drug discovery; drug design.
XX
OS Homo sapiens.
XX
PN WO200142277-A2.
XX
PD 14-JUN-2001.
XX
PF 13-DEC-2000; 2000MO-GB04776.
XX
PR 13-DEC-1999; 99GB-0029464.
XX
PA (PROT-) PROTEOM LTD.
XX
PI Roberts GW, Heal JR;
XX
DR WPI; 2001-408419/43.
XX
A set of peptide ligands consisting of specific complementary peptides
PT to proteins encoded by genes of the human genome, useful in an assay
PT for screening and identifying of one or more novel peptides which are
PT drug candidates or pro-drugs -
XX
PS Example 4; Page 243; 646pp; English.
XX
CC The invention relates to a set of complementary peptide ligands
CC generated from the human genome. The complementary peptides
CC interact with their relevant target proteins encoded in the human
CC genome. They can be used as reagents in drug discovery and as lead
CC ligands to facilitate drug design and development. The present
CC sequence is a complementary peptide provided in the specification.
XX
SQ Sequence 10 AA;

Query Match          52.2%; Score 24; DB 22; Length 10;
Best Local Similarity 83.3%; Pred. No. 3.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 KSOLVK 8
   |||: ||
Db 1 KSOLVK 6

RESULT 12
ABG35074
ID ABG35074 standard; Peptide; 9 AA.
XX
AC ABG35074;
XX
```

```

DT      15-JUL-2002 (first entry)
XX
DE      Hodgkin's disease viral targeting peptide #5.
XX
KW      Targeting peptide; cancer; Hodgkin's disease; cytostatic;
KW      immunosuppressive; anti-inflammatory; antiarthritic; antiviral;
KW      antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;
KW      inflammatory disease; arthritis; atherosclerosis; cancer;
KW      autoimmune disease; bacterial infection; viral infection.
XX
OS      Virididae.
XX
PN      MO200220722-A2.
PD
PE      14-MAR-2002.
PF
PR      07-SEP-2001; 2001WO-US27702.
PR
PR      08-SEP-2000; 2000US-231266P.
PR      17-JAN-2001; 2001US-0765101.
PA      (TEXA ) UNIV TEXAS SYSTEM.
PI      Arap W, Pasqualini R;
PI
PI      WPI; 2002-383050/41.
XX
XX      Identifying targeting peptides useful for treating e.g. diabetes
PT      mellitus, inflammatory diseases, cancer, or autoimmune diseases.
PT      comprises exposing a sample to a phage display library and recovering
PT      phage bound to the sample -
XX
PS      Claim 56; Page 260; 298pp; English.
XX
XX      This invention relates to a novel method for identifying disease
CC      targeting peptides. The method comprises exposing a sample from an
CC      organ, tissue or cell type of interest, to a phage display library and
CC      recovering phage bound to the sample (the phage expresses targeting
CC      peptides). The peptides identified by the method of the invention may
CC      have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,
CC      antiatherosclerotic, antidiabetic, antibacterial and antiviral
CC      activities. The method and composition are useful for identifying
CC      targeting peptides and one or more receptors for a targeting peptide.
CC      The targeting peptides are used for selective delivery of therapeutic
CC      agents, including gene therapy vectors and fusion proteins, to specific
CC      organs, tissues, or cell types in subject. The targeting peptide may
CC      also be used for treating diseases such as diabetes mellitus,
CC      inflammatory diseases, arthritis, atherosclerosis, cancer, autoimmune
CC      diseases, bacterial and viral infections and Hodgkin's disease. The
CC      present sequence represents a targeting peptide of the invention.
SQ
SQ      Sequence      9 AA;
OY      6 LVKRR 10
DB      3 LVKRR 7
OY      |||||
DB      |||||
OY      50.0%; Score 23; DB 23; Length 9;
DB      100.0%; Pred. No. 7.8e+05;
OY      Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DB      3 LVKRR 7
OY
DB

RESULT 13
ID      AAR90268
ID      AAR90268 standard; peptide; 10 AA.
XX
XX      AAR90268;
XX
DT      10-JUL-1996 (first entry)
XX
DE      Ion-channel forming peptide #129 with lipophilic N-terminal group.
XX
KW      Ion channel forming peptide; lipophilic; N-terminal modification;

```

KM	magaatin inhibition; cell growth; viral replication; ionophore;
KM	membrane permeability; antimicrobial; antibacterial; antibiotic;
KM	anti-fungal; anti-viral; spermicidal; anti-tumour; anti-parasitic.
XX	Synthetic.
OS	
XX	
FH	Key
FT	Modified-site
FT	/note= "N-terminal amino group is mono- or
FT	d1-substd. by lipophilic moiety, esp.
FT	octanoyl"
XX	
PN	W09519370-A1.
XX	
XX	
PD	20-JUL-1995.
XX	
PF	18-JAN-1995; 95WO-US00714.
XX	
PR	18-JAN-1994; 94US-0184462.
PA	(MAGA-) MAGALININ PHARM INC.
PI	Kari UP, McLane M, Williams TV;
XX	
DR	WPI; 1995-263826/34.
XX	
PT	Ion channel-forming amphiphilic peptide(s) with N-terminal
PT	lipophilic gps. - useful e.g. as antiviral, antibacterial,
PT	antiparasitic or antitumour agents
PS	
XX	Claim 30; Page 113; 139pp; English.
CC	The present peptide is a specific example corresp. to a highly
CC	generic formula for ion channel forming peptides (ionophores).
CC	These ionophores are known to have a broad range of potent
CC	antibiotic activity against microorganisms including gram-positive
CC	and gram-negative bacteria, fungi, viruses, protozoa and parasites.
CC	N-terminal modification (pref. mono-substn. by octanoyl) to produce
CC	an ion-channel forming peptide having a lipophilic N-terminus
CC	increases the biological activity of the peptides against target cells,
CC	viruses and virally-infected cells, compared to peptides substd. with
CC	an acetyl group at the N-terminus. Compositions comprising the peptides
CC	with lipophilic modifications are claimed for inhibiting growth of a
CC	target cell, virus or virally-infected cell.
XX	
SO	Sequence 10 AA;
	Query Match 50.0%; Score 23; DB 16; Length 10;
	Best Local Similarity 44.4%; Pred. No. 5.7e+02;
	Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
OY	1 KTKSGLVVR 9
	: : :
Db	1 KTKKKFLVK 9
ID	AAI10768 standard; peptide; 10 AA.
XX	AAI10768
AC	AAI10768;
XX	
DT	11-MAY-1999 (first entry)
XX	
DE	Peptide used to make biologically active peptides.
XX	
KX	Septals; septic shock; Pseudomonas aeruginosa; cystic fibrosis;
KM	antimicrobial; antiviral; antibacterial; antifungal; antitumour;
KM	antiparasitic; spermicide; preservative; sterilant; disinfectant;
KM	wound healing; burn; skin infection; eye infection; solid tumour;
KM	leukaemia; non-small cell lung cancer; adenocarcinoma; plant infection;
KM	periodontal disease; plaque; gingivitis; caries; Streptococcus mutans.

OS Synthetic.
 XX WO9903488-A2.
 XX 28-JAN-1999.
 XX 15-JUL-1998; 98WO-US14610.
 XX 15-JUL-1997; 97US-0893006.
 XX (MAGA-) MAGALININ PHARM INC.
 XX Kari UP, McLane M, Williams TJ;
 XX WPI, 1999-131859/11.
 XX Treating sepsis or septic shock with N-modified ion-channel forming
 PT peptide - or its methane sulphonate derivative of reduced toxicity,
 PT also generally useful as antimicrobial and antitumour agents
 XX Example 1; Page 192; 202pp; English.
 XX AA10640-795 represent peptides used in the production of biologically
 CC active peptides with reduced toxicity. The biologically active peptides
 CC are used to treat sepsis or septic shock, and comprise the formula:
 CC T-N(W)-X, where X = biologically active, amphipathic, ion-channel
 CC forming peptide or protein; T = lipophilic group; and W = hydrogen or T.
 CC The peptides are particularly used to treat infections by Pseudomonas
 CC aeruginosa in patients with cystic fibrosis, but more generally as
 CC anti-microbial, antiviral, antibacterial, antifungal, antitumour or
 CC antiparasitic agents, and also as spermicides, e.g. as preservatives,
 CC sterilants, and disinfectants in human and veterinary medicine. They
 CC can be used to stimulate wound healing, treat burns and/or skin and
 CC burn infections, eye infections, solid tumours or leukaemia
 CC (particularly non-small cell lung cancer and adenocarcinoma, including
 CC those resistant to other antitumour agents), and also for treatment of
 CC infections in plants, and, when formulated in oral hygiene formulations,
 CC for treating or preventing periodontal disease, plaque, gingivitis and/or
 CC caries (specifically by action on Streptococcus mutans).
 XX Sequence 10 AA;
 SQ
 Query Match 50.0%; Score 23; DB 20; Length 10;
 Best Local Similarity 44.4%; Pred. No. 5.7e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KXKSQLYKR 9
 Db 1 KXKXKFLKK 9
 RESULT 15
 AAE22481
 ID AAE22481 standard; peptide; 10 AA.
 XX AAE22481;
 XX 25-JUL-2002 (first entry)
 XX Biologically active peptide #113.
 XX Biologically active peptide; toxicity; antimicrobial; anti-tumour;
 KW methane sulphonate derivative; wound healing; burn; therapy; sepsis;
 KW eye infection; cyst; spore; trophozoite; tumour; lung infection;
 KW cystic fibrosis; septic shock; bacterial endotoxin; cytostatic;
 KW antibacterial; immunosuppressive.
 XX Unidentified.
 XX OS
 XX Key Location/Qualifiers
 FT Modified-site 1 /note= "Linked to octanoyl group"
 FT Modified-site 10

FT /note= "C-terminal amide"
 XX US6348445-B1.
 XX 19-FEB-2002.
 XX 15-JUL-1998; 98US-0115737.
 XX 18-JAN-1994; 94US-0184462.
 PR 01-JUN-1992; 92US-0891201.
 PR 05-JUN-1995; 95US-0465330.
 PR 15-JUL-1997; 97US-0893006.
 XX (MAGA-) MAGALININ PHARM INC.
 XX Kari UP, Williams TJ, McLane M;
 XX WPI, 2002-350076/38.
 XX Reducing toxicity of unsubstituted or N-terminal substituted peptide
 PT having antimicrobial and antitumor activity useful in treating e.g.
 PT infections and tumor, by forming methane sulfonate derivative or analog
 PT of peptide -
 XX Example 1; Column 107-108; 78pp; English.
 XX The invention relates to biologically active peptides with reduced
 CC toxicity and methods of preparing them. The peptides and proteins of
 CC the invention have improved antimicrobial and anti-tumour activity
 CC while exhibiting reduced toxicity. The method of reducing toxicity
 CC involves the formation of related methane sulphonate derivatives or
 CC analogues. The method is useful for reducing the toxicity of an
 CC unsubstituted peptide or an N-terminal substituted peptide which is
 CC utilized in promoting or stimulating healing of a wound in a host,
 CC treatment of external burns, prevention or treatment of eye infections
 CC caused by bacteria or fungi, in killing cysts, spores, or trophozoites
 CC of infection-causing organisms, and may also be employed in the
 CC treatment of tumours, serious lung infections such as those occurring
 CC in cystic fibrosis, for treating sepsis, septic shock, and other
 CC related ailments, and for neutralising bacterial endotoxins. The
 CC present sequence is a biologically active peptide of the invention.
 XX Sequence 10 AA;
 SQ
 Query Match 50.0%; Score 23; DB 23; Length 10;
 Best Local Similarity 44.4%; Pred. No. 5.7e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 KXKSQLYKR 9
 Db 1 KXKXKFLKK 9
 Search completed: February 8, 2003, 11:03:09
 Job time : 36 secs

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OM protein - protein search, using sw model

Run on: February 8, 2003, 11:04:07 ; Search time 11 Seconds
(without alignments)
20.154 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KXKSQLVYRK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 129505 seqs, 22169297 residues

Total number of hits satisfying chosen parameters: 23513

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Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubppaa/PCR_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:*
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- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	43.5	9	US-09-878-603-14	Sequence 14, Appl
2	20	43.5	9	US-09-779-308-182	Sequence 182, App
3	20	43.5	9	US-09-779-308-481	Sequence 481, App
4	20	43.5	10	US-09-819-308-46	Sequence 46, Appl
5	20	43.5	10	US-09-877-804-22	Sequence 22, Appl
6	19	41.3	7	US-10-147-454-6	Sequence 6, Appl
7	19	41.3	8	US-09-243-079-26	Sequence 26, Appl
8	19	41.3	9	US-09-878-603-20	Sequence 20, Appl
9	19	41.3	9	US-09-805-301-1	Sequence 1, Appl
10	19	41.3	10	US-09-520-698-1	Sequence 1, Appl
11	19	41.3	10	US-09-520-698-5	Sequence 5, Appl
12	19	41.3	10	US-09-520-698-6	Sequence 6, Appl
13	19	41.3	10	US-10-100-057-15	Sequence 15, Appl
14	18	39.1	6	US-09-867-852-205	Sequence 205, App
15	18	39.1	6	US-09-867-852-207	Sequence 207, App
16	18	39.1	7	US-09-789-996-42	Sequence 42, Appl
17	18	39.1	7	US-09-798-116-19	Sequence 19, Appl
18	18	39.1	8	US-09-752-533-2	Sequence 2, Appl
19	18	39.1	9	US-09-878-603-21	Sequence 21, Appl

20	18	39.1	9	US-09-765-527-220	Sequence 220, App
21	18	39.1	9	US-09-834-765-18	Sequence 18, Appl
22	18	39.1	9	US-09-834-765-219	Sequence 219, App
23	18	39.1	9	US-09-834-765-331	Sequence 331, App
24	18	39.1	9	US-09-752-533-3	Sequence 3, Appl
25	18	39.1	9	US-09-918-243-47	Sequence 47, Appl
26	18	39.1	9	US-09-905-083-47	Sequence 47, Appl
27	18	39.1	9	US-09-779-308-211	Sequence 211, App
28	18	39.1	10	US-09-838-785-24	Sequence 24, Appl
29	18	39.1	10	US-09-124-280A-16	Sequence 16, Appl
30	18	39.1	10	US-09-752-533-4	Sequence 4, Appl
31	18	39.1	10	US-09-752-533-7	Sequence 7, Appl
32	18	39.1	10	US-09-779-308-63	Sequence 63, Appl
33	17	37.0	7	US-09-989-789-208	Sequence 208, App
34	17	37.0	7	US-09-989-789-211	Sequence 211, App
35	17	37.0	7	US-09-989-789-213	Sequence 213, App
36	17	37.0	7	US-09-989-789-214	Sequence 214, App
37	17	37.0	7	US-09-989-789-216	Sequence 216, App
38	17	37.0	7	US-09-989-789-222	Sequence 222, App
39	17	37.0	8	US-09-243-079-27	Sequence 27, Appl
40	17	37.0	8	US-09-243-079-48	Sequence 48, Appl
41	17	37.0	8	US-09-883-825-2	Sequence 2, Appl
42	17	37.0	9	US-09-957-909-2	Sequence 2, Appl
43	17	37.0	9	US-09-178-286-7	Sequence 7, Appl
44	17	37.0	9	US-10-211-207-1	Sequence 1, Appl
45	17	37.0	9	US-10-211-207-15	Sequence 15, Appl

ALIGNMENTS

RESULT 1
US-09-878-603-14
Sequence 14, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarna, Vidya
APPLICANT: Czernak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: US-03783
CURRENT APPLICATION NUMBER: US/09/878,603
PRIOR FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-878-603-14

Query Match 43.5%; Score 20; DB 9; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.1e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KXKSQLVYRK 9
Db 1 KXKSQLVYRK 9

RESULT 2
US-09-779-308-182
Sequence 182, Application US/09779308
Patent No. US20020150972A1
GENERAL INFORMATION:
APPLICANT: Mary Paris
APPLICANT: Daniel E.H. Afar
APPLICANT: Pia M. Chailita-Eid
APPLICANT: Rene S. Hubert
APPLICANT: Eliana Levin

```
/ APPLICANT: Steve Chappell Mitchell
/ APPLICANT: Aya Jakobovits
/ TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.4USU1
/ CURRENT APPLICATION NUMBER: US/09/779,308
/ PRIOR FILING DATE: 2001-02-08
/ PRIOR APPLICATION NUMBER: 60/181,020
/ NUMBER OF SEQ ID NOS: 718
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 182
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-779-308-182

Query Match      43.5%; Score 20; DB 10; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.1e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy      1 KXKSOLVKR 9
Db      1 KIKKSSSKR 9

RESULT 3
US-09-779-308-481
/ Sequence 481, Application US/09779308
/ Patent No. US20020150972A1
/ GENERAL INFORMATION:
/ APPLICANT: Mary Paris
/ APPLICANT: Daniel E.H. Afar
/ APPLICANT: Pia M. Challita-Bid
/ APPLICANT: Rene S. Hubert
/ APPLICANT: Eliana Levin
/ APPLICANT: Steve Chappell Mitchell
/ TITLE OF INVENTION: 34P3D7: A TISSUE SPECIFIC PROTEIN
/ TITLE OF INVENTION: HIGHLY EXPRESSED IN PROSTATE CANCER
/ FILE REFERENCE: 129.4USU1
/ CURRENT APPLICATION NUMBER: US/09/779,308
/ CURRENT FILING DATE: 2001-02-08
/ PRIOR APPLICATION NUMBER: 60/181,020
/ PRIOR FILING DATE: 2000-02-08
/ NUMBER OF SEQ ID NOS: 718
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 481
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-09-779-308-481

Query Match      43.5%; Score 20; DB 10; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.1e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Oy      1 KXKSOLVKR 9
Db      1 KIKKSSSKR 9

RESULT 4
US-09-819-308-46
/ Sequence 46, Application US/09819308
/ Patent No. US20020019040A1
/ GENERAL INFORMATION:
/ APPLICANT: No. US20020019040A1edorn, Machleu
/ APPLICANT: Damen-van Oorschot, Astrid
/ APPLICANT: Rohn, Jennifer
/ TITLE OF INVENTION: APOPTIN-ASSOCIATING PROTEIN
/ FILE REFERENCE: 2906-4820US
/ CURRENT APPLICATION NUMBER: US/09/819,308
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/ CURRENT FILING DATE: 2001-03-27
/ NUMBER OF SEQ ID NOS: 46
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 46
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Sequence homology analysis of BRP1
US-09-819-308-46

Query Match      43.5%; Score 20; DB 10; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Oy      6 LVKRR 10
Db      3 LVKRR 7

RESULT 5
US-09-877-804-22
/ Sequence 22, Application US/09877804
/ Patent No. US20020061557A1
/ GENERAL INFORMATION:
/ APPLICANT: Nikolics, Karoly
/ APPLICANT: McFarland, Keith C.
/ APPLICANT: Segalo, Deborah L.
/ APPLICANT: Seeburg, Peter H.
/ TITLE OF INVENTION: Glycoprotein Hormone Receptor Molecules
/ FILE REFERENCE: P0576P1C2
/ CURRENT APPLICATION NUMBER: US/09/877,804
/ CURRENT FILING DATE: 2001-09-04
/ PRIOR APPLICATION NUMBER: US 08/207,814
/ PRIOR FILING DATE: 1994-03-07
/ PRIOR APPLICATION NUMBER: US 07/781,153
/ PRIOR FILING DATE: 1991-10-31
/ PRIOR APPLICATION NUMBER: US 07/347,683
/ PRIOR FILING DATE: 1989-05-05
/ NUMBER OF SEQ ID NOS: 22
/ SEQ ID NO 22
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Fragment
US-09-877-804-22

Query Match      43.5%; Score 20; DB 10; Length 10;
Best Local Similarity 37.5%; Pred. No. 2.9e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Oy      3 KSOLVKRR 10
Db      1 RAELVKRR 8

RESULT 6
US-10-147-454-6
/ Sequence 6, Application US/10147454
/ Publication No. US20020193308A1
/ GENERAL INFORMATION:
/ APPLICANT: NAKTINIS, Vytautas
/ APPLICANT: CONCAS BENEVELLI, Daniela
/ APPLICANT: BERRA, Bruno
/ APPLICANT: COLOMBO, Irma
/ APPLICANT: RONCHI, Severino
/ APPLICANT: BARTORELLI, Alberto
/ APPLICANT: BUNELIS, Viadas Algirdus
/ TITLE OF INVENTION: Recombinant Protein and Its Use in Therapy and Diagnostics
/ FILE REFERENCE: 0471-0273P
/ CURRENT APPLICATION NUMBER: US/10/147,454
/ CURRENT FILING DATE: 2002-05-17
/ NUMBER OF SEQ ID NOS: 9
/ SOFTWARE: PatentIn version 3.1
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SEQ ID NO 6
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 5' end of the amino acid sequence derived from the coding region
OTHER INFORMATION: of the UK14 cDNA sequence derived from Capra hircus
US-10-147-454-6

Query Match 41.3%; Score 19; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.1e+05;
Matches 4; Conservative 1; Mismatches 1; Gaps 0;

QY 4 SOLVLR 9
DB 2 SSVLR 7

RESULT 7
US-09-243-079-26
Sequence 26, Application US/09243079
Patent No. US20020081566A1
GENERAL INFORMATION:
APPLICANT: Beretta, Alberto
TITLE OF INVENTION: HIV PROTEIN EPITOPES IMMUNOLOGICALLY
FILE REFERENCE: 29928-PCT-USA-1
CURRENT APPLICATION NUMBER: US/09/243,079
CURRENT FILING DATE: 1999-02-02
PRIOR APPLICATION NUMBER: 08/335,733
PRIOR FILING DATE: 1994-11-10
PRIOR APPLICATION NUMBER: PCT/IT93/00049
PRIOR FILING DATE: 1993-05-10
PRIOR APPLICATION NUMBER: RM92A/000350
PRIOR FILING DATE: 1992-05-11
NUMBER OF SEQ ID NOS: 89
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 26
LENGTH: 8
TYPE: PRT
ORGANISM: Human Immunodeficiency Virus
US-09-243-079-26

Query Match 41.3%; Score 19; DB 10; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KSQLVKK 10
DB 1 RSELYKK 8

RESULT 8
US-09-878-603-20
Sequence 20, Application US/09878603
Patent No. US20020165138A1
GENERAL INFORMATION:
APPLICANT: Ward, Peter A.
APPLICANT: Huber-Lang, Markus
APPLICANT: Sarmak, Vldya
APPLICANT: Czeizmak, Boris
TITLE OF INVENTION: Compositions and Methods for the Treatment of Sepsis
FILE REFERENCE: UM-03783
CURRENT APPLICATION NUMBER: US/09/878,603
CURRENT FILING DATE: 2001-06-11
PRIOR APPLICATION NUMBER: 09/387,671
PRIOR FILING DATE: 1999-08-31
NUMBER OF SEQ ID NOS: 74
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 20
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-878-603-20

Query Match 41.3%; Score 19; DB 9; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.1e+05;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 KLSQVLR 9
DB 1 KYKHTVKK 9

RESULT 9
US-09-805-301-1
Sequence 1, Application US/09805301
Patent No. US20020173456A1
GENERAL INFORMATION:
APPLICANT: Smith, Louis C.
Sparrow, James T.
Hauer, Jocheen
Mims, Martha P.
TITLE OF INVENTION: LIPOPHILIC PEPTIDES FOR
MACROMOLECULE DELIVERY
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 6.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/805,301
FILING DATE: 12-Mar-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/584,043
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wardburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 217/189
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
MOLECULE TYPE: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-805-301-1

Query Match 41.3%; Score 19; DB 9; Length 9;
Best Local Similarity 37.5%; Pred. No. 1.1e+05;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLSQVLR 8
DB 2 KLRKRLR 9

RESULT 10
US-09-520-698-1
; Sequence 1, Application US/09520698
; Patent No. US20020128175A1
; GENERAL INFORMATION:
; APPLICANT: Gattadahalil M. Anantharamaiah
; TITLE OF INVENTION: Synthetic Peptides that Enhance LDL Uptake
; FILE REFERENCE: D6084
; CURRENT APPLICATION NUMBER: US/09/520,698
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: 09/271,066
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 1
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: 141..150
; OTHER INFORMATION: minimal arginine-rich human apolipoprotein E
; OTHER INFORMATION: receptor binding domain
US-09-520-698-1

Query Match 41.3%; Score 19; DB 10; Length 10;
Best Local Similarity 37.5%; Pred. No. 4.4e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLSQLVK 8
||:|:|:
Db 3 KLRKRLR 10

RESULT 11
US-09-520-698-5
; Sequence 5, Application US/09520698
; Patent No. US20020128175A1
; GENERAL INFORMATION:
; APPLICANT: Gattadahalil M. Anantharamaiah
; TITLE OF INVENTION: Synthetic Peptides that Enhance LDL Uptake
; FILE REFERENCE: D6084
; CURRENT APPLICATION NUMBER: US/09/520,698
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: 09/271,066
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 5
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Lepus sp.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: 134..143
; OTHER INFORMATION: rabbit apolipoprotein E receptor binding domain
US-09-520-698-5

Query Match 41.3%; Score 19; DB 10; Length 10;
Best Local Similarity 37.5%; Pred. No. 4.4e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLSQLVK 8
||:|:|:
Db 3 KLRKRLR 10

RESULT 12
US-09-520-698-6
; Sequence 6, Application US/09520698
; Patent No. US20020128175A1
; GENERAL INFORMATION:
; APPLICANT: Gattadahalil M. Anantharamaiah
; TITLE OF INVENTION: Synthetic Peptides that Enhance LDL Uptake
; FILE REFERENCE: D6084

; CURRENT APPLICATION NUMBER: US/09/520,698
; CURRENT FILING DATE: 1999-03-17
; PRIOR APPLICATION NUMBER: 09/271,066
; PRIOR FILING DATE: 1998-03-17
; NUMBER OF SEQ ID NOS: 10
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Monkey sp.
; FEATURE:
; NAME/KEY: DOMAIN
; LOCATION: 141..150
; OTHER INFORMATION: monkey apolipoprotein E receptor binding domain
US-09-520-698-6

Query Match 41.3%; Score 19; DB 10; Length 10;
Best Local Similarity 37.5%; Pred. No. 4.4e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLSQLVK 8
||:|:|:
Db 3 KLRKRLR 10

RESULT 13
US-10-100-057-15
; Sequence 15, Application US/10100057
; Patent No. US20020150555A1
; GENERAL INFORMATION:
; APPLICANT: GILLISPIE, Matthew Todd
; HORWOOD, Nicole Joy
; UDAGAWA, No. US20020150555A1uyuki
; KURIMOTO, Masashi
; TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
; NUMBER OF SEQUENCES: 28
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: BROWDY AND NEIMARK
; STREET: 419 Seventh Street, N.W., Suite 300
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/100,057
; FILING DATE: 19-Mar-2002
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/030,061
; FILING DATE: 25-FEB-1998
; APPLICATION NUMBER: JP 55,468/1997
; FILING DATE: 25-FEB-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: BROWDY, Roger L.
; REGISTRATION NUMBER: 25,618
; REFERENCE/DOCKET NUMBER: GILLISPIE-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-5197
; TELEFAX: (202) 737-3528
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal fragment
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-100-057-15

Query Match 41.3%; Score 19; DB 12; Length 10;

Best Local Similarity 66.7%; Pred. No. 4.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 KXKS 6
Db 4 KXKS 9

RESULT 14
US-09-867-852-205
; Sequence 205, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumitaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 205
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-205

Query Match 39.1%; Score 18; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KXKS 4
Db 2 KXKS 5

RESULT 15
US-09-867-852-207
; Sequence 207, Application US/09867852
; Patent No. US20020147324A1
; GENERAL INFORMATION:
; APPLICANT: Ausubel, Frederick M.
; APPLICANT: Staskawicz, Brian J.
; APPLICANT: Brent, Andrew F.
; APPLICANT: Dahlbeck, Douglas
; APPLICANT: Katagiri, Fumitaki
; APPLICANT: Kunkel, Barbara N.
; APPLICANT: Mindrinos, Michael N.
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: RPS2 GENE FAMILY, PRIMERS, PROBES, AND
; FILE REFERENCE: 00786/254002
; CURRENT APPLICATION NUMBER: US/09/867,852
; PRIOR FILING DATE: 2001-05-29
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/301,085
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-04-28
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/310,912
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-09-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 08/227,360
; PRIOR FILING DATE: EARLIER FILING DATE: 1994-04-13

; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 207
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-867-852-207

Query Match 39.1%; Score 18; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.1e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KXKS 4
Db 2 KXKS 5

Search completed: February 8, 2003, 11:07:43
Job time : 12 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 11:03:13 ; Search time 133 Seconds
(without alignments)
48.476 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KXKSQWKRK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 4569144 seqs, 644733110 residues
Total number of hits satisfying chosen parameters: 417449

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3:	/cgn2_6/ptodata/1/paa/US07_COMB.pep.*
4:	/cgn2_6/ptodata/1/paa/US08_COMB.pep.*
5:	/cgn2_6/ptodata/1/paa/US081_COMB.pep.*
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24:	/cgn2_6/ptodata/1/paa/US100_COMB.pep.*
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26:	/cgn2_6/ptodata/1/paa/US102_COMB.pep.*
27:	/cgn2_6/ptodata/1/paa/US60_COMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	46	100.0	10	7	US-08-318-892-4
2	46	100.0	10	23	US-09-685-010-31
3	46	100.0	10	23	US-09-878-309A-31
4	43	93.5	10	7	US-08-318-892B-4
5	43	93.5	10	15	US-09-169-077-2
6	43	93.5	10	18	US-09-424-292-6

7	43	93.5	10	18	US-09-424-292-15	Sequence 15, Appl
8	43	93.5	10	18	US-09-424-292-28	Sequence 28, Appl
9	39	84.8	10	15	US-09-169-077-8	Sequence 8, Appl
10	38	82.6	9	7	US-08-318-892B-32	Sequence 32, Appl
11	38	82.6	9	20	US-09-685-010-59	Sequence 59, Appl
12	38	82.6	9	23	US-09-978-309A-59	Sequence 59, Appl
13	38	82.6	10	7	US-08-318-892-13	Sequence 13, Appl
14	38	82.6	10	7	US-08-318-892B-13	Sequence 13, Appl
15	38	82.6	10	18	US-09-424-292-23	Sequence 23, Appl
16	38	82.6	10	18	US-09-424-292-30	Sequence 30, Appl
17	38	82.6	10	18	US-09-424-292-32	Sequence 32, Appl
18	37	80.4	10	7	US-08-318-892-11	Sequence 11, Appl
19	37	80.4	10	7	US-08-318-892B-11	Sequence 11, Appl
20	37	80.4	10	18	US-09-424-292-31	Sequence 31, Appl
21	36	78.3	10	7	US-08-318-892-12	Sequence 12, Appl
22	36	78.3	10	7	US-08-318-892B-12	Sequence 12, Appl
23	36	78.3	10	18	US-09-424-292-34	Sequence 34, Appl
24	32	69.6	10	18	US-09-424-292-25	Sequence 25, Appl
25	32	69.6	10	18	US-09-424-292-33	Sequence 33, Appl
26	31	67.4	10	15	US-09-169-077-7	Sequence 7, Appl
27	28	60.9	10	7	US-08-318-892-14	Sequence 14, Appl
28	28	60.9	10	7	US-08-318-892B-14	Sequence 14, Appl
29	28	60.9	10	18	US-09-424-292-29	Sequence 29, Appl
30	24	52.2	10	1	PCT-US02-19683-658	Sequence 658, Appl
31	24	52.2	10	19	US-09-572-404B-1412	Sequence 1412, Appl
32	23	50.0	9	1	PCT-US01-27702A-161	Sequence 161, Appl
33	23	50.0	9	18	US-09-424-292-17	Sequence 17, Appl
34	23	50.0	9	21	US-09-765-101-202	Sequence 202, Appl
35	23	50.0	9	27	US-60-231-266-202	Sequence 202, Appl
36	23	50.0	10	8	US-08-404-283-129	Sequence 129, Appl
37	23	50.0	10	8	US-08-465-330-129	Sequence 129, Appl
38	23	50.0	10	8	US-08-474-654-6	Sequence 6, Appl
39	22	47.8	7	24	US-10-006-766-26	Sequence 26, Appl
40	22	47.8	10	1	PCT-US98-10896-50	Sequence 50, Appl
41	22	47.8	10	19	US-09-572-404B-1984	Sequence 1984, Appl
42	22	47.8	10	25	US-10-177-725-134	Sequence 134, Appl
43	21	45.7	8	18	US-09-412-863-3187	Sequence 3187, Appl
44	21	45.7	8	18	US-09-412-863-3563	Sequence 3563, Appl
45	21	45.7	8	18	US-09-412-863-9609	Sequence 9609, Appl

ALIGNMENTS

RESULT 1
US-08-318-892-4
Sequence 4, Application US/08318892
GENERAL INFORMATION:
APPLICANT: Turley, Eva A
TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR
TITLE OF INVENTION: FOR HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING
TITLE OF INVENTION: PEPTIDES
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: C/O FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: N.Y.
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318, 892
FILING DATE: 1-DEC-1994
CLASSIFICATION: 516
ATTORNEY/AGENT INFORMATION:
NAME: Pieriti, Margaret A
REGISTRATION NUMBER: 30,709
REFERENCE/DOCKET NUMBER: SIM-8

```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-318-892-4

Query Match          100.0%; Score 46; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIKSQLVVRK 10
Db 1 KIKSQLVVRK 10

RESULT 2
US-09-685-010-31
; Sequence 31, Application US/09685010
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
;   TITLE OF INVENTION: CELLULAR RESPONSE TO INJURY AND OTHER PROLIFERATING CELL
;   TITLE OF INVENTION: DISORDERS REGULATED BY HYALADHERIN AND HYALURONANS
; FILE REFERENCE: 910130.401C1
; CURRENT APPLICATION NUMBER: US/09/685,010
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide composition that binds a hyalauronan
US-09-685-010-31

Query Match          100.0%; Score 46; DB 20; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIKSQLVVRK 10
Db 1 KIKSQLVVRK 10

RESULT 3
US-09-978-309A-31
; Sequence 31, Application US/09978309A
; GENERAL INFORMATION:
; APPLICANT: Cruz, Tony
; APPLICANT: Pastirik, Alekandra
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
;   TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
;   TITLE OF INVENTION: Hyaladherin and Hyaluronans
; FILE REFERENCE: 033352-010
; CURRENT APPLICATION NUMBER: US/09/978,309A
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 09/685,010
; PRIOR FILING DATE: 2000-10-05
; PRIOR APPLICATION NUMBER: US 09/541,522
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: US 60/127,457
; PRIOR FILING DATE: 1999-04-01
; NUMBER OF SEQ ID NOS: 84
; SOFTWARE: FastSeq for Windows Version 4.0
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; SEQ ID NO 31
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide composition that binds a hyalauronan
US-09-978-309A-31

Query Match          100.0%; Score 46; DB 23; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.11;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIKSQLVVRK 10
Db 1 KIKSQLVVRK 10

RESULT 4
US-08-318-892B-4
; Sequence 4, Application US/0831892B
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A.
; TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR FOR
;   TITLE OF INVENTION: HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING PEPTIDES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: c/o FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,892B
; FILING DATE: 1-DEC-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pietri, Margaret A
; REGISTRATION NUMBER: 30709
; REFERENCE/DOCKET NUMBER: SIM-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 10 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-08-318-892B-4

Query Match          93.5%; Score 43; DB 7; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 KIKSQLVVRK 10
Db 1 KIKSQLVVRK 10

RESULT 5
US-09-169-077-2
; Sequence 2, Application US/09169077
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN HYALURONAN RECEPTOR
; NUMBER OF SEQUENCES: 52
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```
COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,077
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CA97/00240
; FILING DATE:
; APPLICATION NUMBER: GB 9607441.4
; FILING DATE: 10-APR-1996
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-169-077-2
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```
Query Match          93.5%; Score 43; DB 15; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 KLRSQLVYRK 10
Db 1 KLRSQLVYRK 10
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```
RESULT 6
US-09-424-292-6
; Sequence 6, Application US/09424292
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: Improved Delivery of Disease Modifiers
; FILE REFERENCE: 205375
; CURRENT APPLICATION NUMBER: US/09/424,292
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: PCT/CA98/00448
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: CA 2,205,771
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-424-292-6
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```
Query Match          93.5%; Score 43; DB 18; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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```
QY 1 KLRSQLVYRK 10
Db 1 KLRSQLVYRK 10
```

```
RESULT 7
US-09-424-292-15
; Sequence 15, Application US/09424292
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: Improved Delivery of Disease Modifiers
; FILE REFERENCE: 205375
; CURRENT APPLICATION NUMBER: US/09/424,292
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: PCT/CA98/00448
```

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; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: CA 2,205,771
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-424-292-15
```

```
Query Match          93.5%; Score 43; DB 18; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLRSQLVYRK 10
Db 1 KLRSQLVYRK 10
```

```
RESULT 8
US-09-424-292-28
; Sequence 28, Application US/09424292
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: Improved Delivery of Disease Modifiers
; FILE REFERENCE: 205375
; CURRENT APPLICATION NUMBER: US/09/424,292
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: PCT/CA98/00448
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: CA 2,205,771
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-09-424-292-28
```

```
Query Match          93.5%; Score 43; DB 18; Length 10;
Best Local Similarity 90.0%; Pred. No. 0.42;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KLRSQLVYRK 10
Db 1 KLRSQLVYRK 10
```

```
RESULT 9
US-09-169-077-8
; Sequence 8, Application US/09169077
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: HUMAN HYALURONAN RECEPTOR
; NUMBER OF SEQUENCES: 52
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (ERO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/169,077
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/CA97/00240
; FILING DATE:
; APPLICATION NUMBER: GB 9607441.4
```

;; FILING DATE: 10-APR-1996
;; INFORMATION FOR SEQ ID NO: 8:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 10 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-09-169-077-8

Query Match 84.6%; Score 39; DB 15; Length 10;
Best Local Similarity 80.9%; Pred. No. 2.4;
Matches 8; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 KLKSQLVKK 10
Db 1 KLKSQLAKRK 10

RESULT 10
US-08-318-892B-32
; Sequence 32, Application US/08318892B
; GENERAL INFORMATION:

;; APPLICANT: Turley, Eva A
;; TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR FOR
;; TITLE OF INVENTION: HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING PEPTIDES
;; NUMBER OF SEQUENCES: 41
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: C/O FISH & NEAVE
;; STREET: 1251 Avenue of the Americas
;; CITY: New York
;; STATE: N.Y.
;; COUNTRY: USA
;; ZIP: 10020

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,892B

FILING DATE: 1-DEC-1994

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Pierri, Margaret A

REGISTRATION NUMBER: 30709

REFERENCE/DOCKET NUMBER: SIM-8

TELEPHONE: (212) 596-9000

TELEFAX: (212) 596-9090

INFORMATION FOR SEQ ID NO: 32:

SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-318-892B-32

Query Match 82.6%; Score 38; DB 7; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLKSQLVKK 9
Db 1 KLKSQLVKK 9

RESULT 11
US-09-685-010-59
; Sequence 59, Application US/09685010
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A.

;; APPLICANT: Cruz, Tony F
;; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
;; TITLE OF INVENTION: CELLULAR RESPONSE TO INJURY AND OTHER PROLIFERATING CELL
;; TITLE OF INVENTION: DISORDERS REGULATED BY HYALADHERIN AND HYALURONANS
;; FILE REFERENCE: 910130.401C1
;; CURRENT APPLICATION NUMBER: US/09/685,010
;; NUMBER OF SEQ ID NOS: 72
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 59
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: Homo sapien
US-09-685-010-59

Query Match 82.6%; Score 38; DB 20; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLKSQLVKK 9
Db 1 KLKSQLVKK 9

RESULT 12
US-09-978-309A-59
; Sequence 59, Application US/09978309A
; GENERAL INFORMATION:

;; APPLICANT: Cruz, Tony
;; APPLICANT: Pastrak, Aleksandra
;; TITLE OF INVENTION: Compositions and Methods for Treating Cellular Response to
;; TITLE OF INVENTION: Injury and Other Proliferating Cell Disorders Regulated by
;; TITLE OF INVENTION: Hyaladerin and Hyaluronans
;; FILE REFERENCE: 033352-010
;; CURRENT APPLICATION NUMBER: US/09/978,309A

CURRENT FILING DATE: 2002-04-04

PRIOR APPLICATION NUMBER: US 09/685,010

PRIOR FILING DATE: 2000-10-05

PRIOR APPLICATION NUMBER: US 09/541,522

PRIOR FILING DATE: 2000-04-03

PRIOR APPLICATION NUMBER: US 60/127,457

PRIOR FILING DATE: 1999-04-01

NUMBER OF SEQ ID NOS: 84

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 59

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapien

US-09-978-309A-59

Query Match 82.6%; Score 38; DB 23; Length 9;
Best Local Similarity 88.9%; Pred. No. 4.2e+06;
Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KLKSQLVKK 9
Db 1 KLKSQLVKK 9

RESULT 13
US-08-318-892-13
; Sequence 13, Application US/08318892
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR
; TITLE OF INVENTION: FOR HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York


```

; STATE: N.Y.
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WordPerfect 6.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,892
; FILING DATE: 1-DEC-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pierri, Margaret A
; REGISTRATION NUMBER: 30,709
; REFERENCE/DOCKET NUMBER: SIM-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9000
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-318-892-13

```

```

Query Match      82.6%; Score 38; DB 7; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

```

```

QY      2 LKSQLVVRK 10
Db      2 LKSQLVVRK 10

```

```

RESULT 14
US-08-318-892B-13
; Sequence 13, Application US/08318892B
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: HYALURONAN RECEPTOR (RHAMM = RECEPTOR FOR
; TITLE OF INVENTION: HYALURONAN MEDIATED MOBILITY) AND HYALURONAN BINDING PEPTIDES
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: C/O FISH & NEAVE
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: N.Y.
; COUNTRY: USA
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,892B
; FILING DATE: 1-DEC-1994
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Pierri, Margaret A
; REGISTRATION NUMBER: 30709
; REFERENCE/DOCKET NUMBER: SIM-8
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 596-9090
; TELEFAX: (212) 596-9090
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single

```

```

; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-318-892B-13

```

```

Query Match      82.6%; Score 38; DB 7; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

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```

QY      2 LKSQLVVRK 10
Db      2 LKSQLVVRK 10

```

```

RESULT 15
US-09-424-292-23
; Sequence 23, Application US/09424292
; GENERAL INFORMATION:
; APPLICANT: Turley, Eva A
; TITLE OF INVENTION: Improved Delivery of Disease Modifiers
; FILE REFERENCE: 205375
; CURRENT APPLICATION NUMBER: US/09/424,292
; CURRENT FILING DATE: 2000-07-06
; PRIOR APPLICATION NUMBER: PCT/CA98/00448
; PRIOR FILING DATE: 1998-05-11
; PRIOR APPLICATION NUMBER: CA 2,205,771
; PRIOR FILING DATE: 1997-05-22
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 23
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
; US-09-424-292-23

```

```

Query Match      82.6%; Score 38; DB 18; Length 10;
Best Local Similarity 88.9%; Pred. No. 3.7;
Matches 8; Conservative 1; Mismatches 0; Gaps 0;

```

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QY      2 LKSQLVVRK 10
Db      2 LKSQLVVRK 10

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Search completed: February 8, 2003, 11:07:01
Job time : 134 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 8, 2003, 11:03:32 ; Search time 18 Seconds
(without alignments)
45.044 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KLSQVWKRK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 405691 seqs, 81078759 residues

Total number of hits satisfying chosen parameters: 98588

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : Pending Patents_AA_New:*
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*
3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*
4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*
5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*
6: /cgn2_6/ptodata/2/paa/US10_NEW_COMB.pep:*
7: /cgn2_6/ptodata/2/paa/US60_NEW_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	23	50.0	9	US-09-641-528-2553	Sequence 2553, Ap
2	23	50.0	9	US-09-641-528-24854	Sequence 24854, A
3	23	50.0	9	US-09-641-528A-2553	Sequence 2553, Ap
4	23	50.0	9	US-09-641-528A-24854	Sequence 24854, A
5	23	50.0	10	US-09-641-528-18049	Sequence 18049, A
6	23	50.0	10	US-09-641-528-24855	Sequence 24855, A
7	23	50.0	10	US-09-641-528A-18049	Sequence 18049, A
8	23	50.0	10	US-09-641-528A-24855	Sequence 24855, A
9	22	47.8	8	US-09-641-528-2124	Sequence 2124, Ap
10	22	47.8	8	US-09-641-528-4864	Sequence 4864, Ap
11	22	47.8	8	US-09-641-528-9364	Sequence 9364, Ap
12	22	47.8	8	US-09-641-528-10109	Sequence 10109, A
13	22	47.8	8	US-09-641-528-11706	Sequence 11706, A
14	22	47.8	8	US-09-641-528-24492	Sequence 24492, A
15	22	47.8	8	US-09-641-528-24553	Sequence 24553, A
16	22	47.8	8	US-09-641-528-26751	Sequence 26751, A
17	22	47.8	8	US-09-641-528-26800	Sequence 26800, A
18	22	47.8	8	US-09-641-528-31258	Sequence 31258, A
19	22	47.8	8	US-09-641-528-34284	Sequence 34284, A
20	22	47.8	8	US-09-641-528-39620	Sequence 39620, A
21	22	47.8	8	US-09-641-528-41648	Sequence 41648, A
22	22	47.8	8	US-09-641-528A-2124	Sequence 2124, Ap
23	22	47.8	8	US-09-641-528A-4864	Sequence 4864, Ap
24	22	47.8	8	US-09-641-528A-9364	Sequence 9364, Ap
25	22	47.8	8	US-09-641-528A-10109	Sequence 10109, A
26	22	47.8	8	US-09-641-528A-11706	Sequence 11706, A

27	22	47.8	8	US-09-641-528A-24492	Sequence 24492, A
28	22	47.8	8	US-09-641-528A-24553	Sequence 24553, A
29	22	47.8	8	US-09-641-528A-26751	Sequence 26751, A
30	22	47.8	8	US-09-641-528A-26800	Sequence 26800, A
31	22	47.8	8	US-09-641-528A-31258	Sequence 31258, A
32	22	47.8	8	US-09-641-528A-34284	Sequence 34284, A
33	22	47.8	8	US-09-641-528A-39620	Sequence 39620, A
34	22	47.8	8	US-09-641-528A-41648	Sequence 41648, A
35	22	47.8	9	US-09-641-528-3	Sequence 3, Appl1
36	22	47.8	9	US-09-641-528-697	Sequence 697, App
37	22	47.8	9	US-09-641-528-2125	Sequence 2125, Ap
38	22	47.8	9	US-09-641-528-2181	Sequence 2181, Ap
39	22	47.8	9	US-09-641-528-4924	Sequence 4924, Ap
40	22	47.8	9	US-09-641-528-9374	Sequence 9374, Ap
41	22	47.8	9	US-09-641-528-10125	Sequence 10125, A
42	22	47.8	9	US-09-641-528-11535	Sequence 11535, A
43	22	47.8	9	US-09-641-528-13498	Sequence 13498, A
44	22	47.8	9	US-09-641-528-24299	Sequence 24299, A
45	22	47.8	9	US-09-641-528-24493	Sequence 24493, A

ALIGNMENTS

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RESULT 1
US-09-641-528-2553
; Sequence 2553, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Basteen
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; PRIOR FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2553
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-2553
Query Match 50.0%; Score 23; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
Oy 3 KSQLVWKRK 10
Db 1 KQLVWKRK 8
RESULT 2
US-09-641-528-24854
; Sequence 24854, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Basteen
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
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/ CURRENT APPLICATION NUMBER: US/09/641,528
/ PRIOR FILING DATE: 2000-08-15
/ PRIOR APPLICATION NUMBER: US 60/172,705
/ PRIOR FILING DATE: 1999-12-10
/ NUMBER OF SEQ ID NOS: 51504
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 24854
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-24854

Query Match          50.0%; Score 23; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      3 KSQVKKR 10
       |::|:
Db      1 KQQLRRR 8

RESULT 3
US-09-641-528A-2553
/ Sequence 2553, Application US/09641528A
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Grey, Howard
/ TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
/ TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
/ FILE REFERENCE: 2060.010001
/ CURRENT APPLICATION NUMBER: US/09/641,528A
/ PRIOR FILING DATE: 2000-08-15
/ PRIOR APPLICATION NUMBER: US 60/172,705
/ PRIOR FILING DATE: 1999-12-10
/ NUMBER OF SEQ ID NOS: 51504
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 2553
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528A-2553

Query Match          50.0%; Score 23; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      3 KSQVKKR 10
       |::|:
Db      1 KQQLRRR 8

RESULT 4
US-09-641-528A-24854
/ Sequence 24854, Application US/09641528A
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Grey, Howard
/ TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
/ TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
/ FILE REFERENCE: 2060.010001
/ CURRENT APPLICATION NUMBER: US/09/641,528A
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/ CURRENT FILING DATE: 2000-08-15
/ PRIOR APPLICATION NUMBER: US 60/172,705
/ PRIOR FILING DATE: 1999-12-10
/ NUMBER OF SEQ ID NOS: 51504
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 24854
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528A-24854

Query Match          50.0%; Score 23; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 3.3e+05;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      3 KSQVKKR 10
       |::|:
Db      1 KQQLRRR 8

RESULT 5
US-09-641-528-18049
/ Sequence 18049, Application US/09641528
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Grey, Howard
/ TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
/ TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
/ FILE REFERENCE: 2060.010001
/ CURRENT APPLICATION NUMBER: US/09/641,528
/ PRIOR FILING DATE: 2000-08-15
/ PRIOR APPLICATION NUMBER: US 60/172,705
/ PRIOR FILING DATE: 1999-12-10
/ NUMBER OF SEQ ID NOS: 51504
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 18049
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-18049

Query Match          50.0%; Score 23; DB 5; Length 10;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      3 KSQVKKR 10
       |::|:
Db      2 KQQLRRR 9

RESULT 6
US-09-641-528-24855
/ Sequence 24855, Application US/09641528
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Cells, Esteban
/ APPLICANT: Grey, Howard
/ TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
/ TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
/ FILE REFERENCE: 2060.010001
/ CURRENT APPLICATION NUMBER: US/09/641,528
/ CURRENT FILING DATE: 2000-08-15
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; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24855
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-24855
```

```
Query Match          50.0%; Score 23; DB 5; Length 10;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      3 KSOVYRK 10
        |||::|
Db       1 KQQLRRR 8
```

```
RESULT 7
US-09-641-528A-18049
; Sequence 18049, Application US/09641528A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Beteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528A
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18049
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528A-18049
```

```
Query Match          50.0%; Score 23; DB 5; Length 10;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      3 KSOVYRK 10
        |||::|
Db       2 KQQLRRR 9
```

```
RESULT 8
US-09-641-528A-24855
; Sequence 24855, Application US/09641528A
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Beteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528A
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
```

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; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 24855
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528A-24855
```

```
Query Match          50.0%; Score 23; DB 5; Length 10;
Best Local Similarity 50.0%; Pred. No. 72;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
OY      3 KSOVYRK 10
        |||::|
Db       1 KQQLRRR 8
```

```
RESULT 9
US-09-641-528-2124
; Sequence 2124, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Beteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2124
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-2124
```

```
Query Match          47.8%; Score 22; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3.3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      5 QLVYRK 10
        |||::|
Db       1 QVLRRK 6
```

```
RESULT 10
US-09-641-528-4864
; Sequence 4864, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Cells, Beteban
; APPLICANT: Grey, Howard
; TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.0100001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
```

NUMBER OF SEQ ID NOS: 51504
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 4864
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-4864

Query Match 47.8%; Score 22; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3.3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLVKRX 10
|::|||
Db 1 QLVKRX 6

RESULT 11
US-09-641-528-9364
Sequence 9364, Application US/09641528
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51504
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9364
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-9364

Query Match 47.8%; Score 22; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3.3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLVKRX 10
|::|||
Db 3 QLVKRX 8

RESULT 12
US-09-641-528-10109
Sequence 10109, Application US/09641528
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51504

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10109
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-10109

Query Match 47.8%; Score 22; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3.3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLVKRX 10
|::|||
Db 3 QLVKRX 8

RESULT 13
US-09-641-528-11706
Sequence 11706, Application US/09641528
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51504
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11706
LENGTH: 8
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-11706

Query Match 47.8%; Score 22; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3.3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QLVKRX 10
|::|||
Db 1 QLVKRX 6

RESULT 14
US-09-641-528-24492
Sequence 24492, Application US/09641528
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Chesnut, Robert
APPLICANT: Cells, Esteban
APPLICANT: Grey, Howard
TITLE OF INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
TITLE OF INVENTION: USING PEPTIDE AND NUCLEIC ACID COMPOSITIONS
FILE REFERENCE: 2060.0100001
CURRENT APPLICATION NUMBER: US/09/641,528
CURRENT FILING DATE: 2000-08-15
PRIOR APPLICATION NUMBER: US 60/172,705
PRIOR FILING DATE: 1999-12-10
NUMBER OF SEQ ID NOS: 51504
SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 24492
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-24492

Query Match 47.8%; Score 22; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3.3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QVLRK 10
|:|
Db 1 QVLRK 6

RESULT 15
US-09-641-528-24553
; Sequence 24553, Application US/09641528
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Chesnut, Robert
; APPLICANT: Celis, Esben
; APPLICANT: Grey, Howard
; TITLE OR INVENTION: INDUCING CELLULAR IMMUNE RESPONSES TO HUMAN PAPILLOMAVIRUS
; FILE REFERENCE: 2060.010001
; CURRENT APPLICATION NUMBER: US/09/641,528
; CURRENT FILING DATE: 2000-08-15
; PRIOR APPLICATION NUMBER: US 60/172,705
; PRIOR FILING DATE: 1999-12-10
; NUMBER OF SEQ ID NOS: 51504
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 24553
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide Derived from Human Papillomavirus
US-09-641-528-24553

Query Match 47.8%; Score 22; DB 5; Length 8;
Best Local Similarity 66.7%; Pred. No. 3.3e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 QVLRK 10
|:|
Db 2 QVLRK 7

Search completed: February 8, 2003, 11:07:26
Job time : 19 secs

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OM protein - protein search, using sw model

Run on: February 8, 2003, 11:02:32 ; Search time 14 Seconds
(without alignments)
21.016 Million cell updates/sec

Title: US-09-685-010-31
Perfect score: 46
Sequence: 1 KLSQVLRK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 77191

Minimum DB seq length: 0
Maximum DB seq length: 10

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5A COMB pep: *
2: /cgn2_6/ptodata/1/1aa/5B COMB pep: *
3: /cgn2_6/ptodata/1/1aa/6A COMB pep: *
4: /cgn2_6/ptodata/1/1aa/6B COMB pep: *
5: /cgn2_6/ptodata/1/1aa/PCTUS COMB pep: *
6: /cgn2_6/ptodata/1/1aa/Backlist1 pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	50.0	10	1	US-08-465-325-129 Sequence 129, App
2	23	50.0	10	4	US-09-115-737-129 Sequence 129, App
3	22	47.8	10	2	US-08-666-564-50 Sequence 50, App1
4	22	47.8	10	3	US-08-865-472-50 Sequence 50, App1
5	22	47.8	10	4	US-09-650-438-50 Sequence 50, App1
6	22	47.8	10	5	PCT-US93-12245-50 Sequence 50, App1
7	21	45.7	9	1	US-08-459-064B-29 Sequence 29, App1
8	21	45.7	9	2	US-08-460-421A-29 Sequence 29, App1
9	21	45.7	10	2	US-08-467-202-2 Sequence 2, App1
10	21	45.7	10	2	US-08-666-564-51 Sequence 51, App1
11	21	45.7	10	3	US-08-865-472-51 Sequence 51, App1
12	21	45.7	10	4	US-09-650-438-51 Sequence 51, App1
13	21	45.7	10	5	PCT-US93-12245-51 Sequence 51, App1
14	21	45.7	10	6	5514565-10 Patent No. 5514565
15	20	43.5	8	2	US-08-672-610A-3 Sequence 3, App1
16	20	43.5	8	4	US-08-444-818-494 Sequence 494, App
17	20	43.5	9	2	US-08-635-007-4 Sequence 4, App1
18	20	43.5	9	3	US-09-110-953-4 Sequence 4, App1
19	20	43.5	9	4	US-09-432-879-4 Sequence 4, App1
20	20	43.5	10	1	US-07-755-461A-9 Sequence 9, App1
21	20	43.5	10	1	US-08-315-831A-9 Sequence 9, App1
22	20	43.5	10	2	US-08-662-318-9 Sequence 9, App1
23	20	43.5	10	2	US-08-635-007-5 Sequence 5, App1
24	20	43.5	10	3	US-09-110-953-5 Sequence 5, App1
25	20	43.5	10	3	US-08-139-762A-44 Sequence 44, App1
26	20	43.5	10	3	US-09-139-762A-60 Sequence 60, App1
27	20	43.5	10	4	US-09-432-879-5 Sequence 5, App1

28	20	43.5	10	5	PCT-US95-12509-9 Sequence 9, App1
29	19	41.3	5	6	5187078-16 Patent No. 5187078
30	19	41.3	6	1	US-08-815-688A-6 Sequence 6, App1
31	19	41.3	7	2	US-08-680-326-92 Sequence 92, App1
32	19	41.3	8	1	US-08-178-476A-6 Sequence 6, App1
33	19	41.3	8	3	US-08-335-733D-26 Sequence 26, App1
34	19	41.3	8	4	US-09-083-366-6 Sequence 6, App1
35	19	41.3	9	1	US-08-338-634-29 Sequence 29, App1
36	19	41.3	9	1	US-08-467-083-12 Sequence 12, App1
37	19	41.3	9	1	US-08-414-417B-12 Sequence 12, App1
38	19	41.3	9	2	US-08-466-348A-12 Sequence 12, App1
39	19	41.3	9	2	US-08-468-545B-12 Sequence 12, App1
40	19	41.3	9	3	US-08-159-339A-273 Sequence 273, App
41	19	41.3	9	3	US-08-159-339A-527 Sequence 527, App
42	19	41.3	9	3	US-08-466-680B-12 Sequence 12, App1
43	19	41.3	9	4	US-08-584-043A-1 Sequence 1, App1
44	19	41.3	10	2	US-08-764-640-60 Sequence 60, App1
45	19	41.3	10	2	US-09-174-060-19 Sequence 19, App1

ALIGNMENTS

RESULT 1
US-08-465-325-129
Sequence 129, Application US/08465325
Patent No. 568563
GENERAL INFORMATION:
APPLICANT: Magalini Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: Plymouth Meeting, PA 19462
TITLE OF INVENTION: Biologically Active Peptides Having
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunner
STREET: 1300 I. Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,325
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0021-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4000
INFORMATION FOR SEQ ID NO: 129:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-325-129

Query Match 50.0%; Score 23; DB 1; Length 10;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 1 KUKSOLVKR 9
Db 1 KUKKFKLK 9

RESULT 2
US-09-115-737-129
; Sequence 129, Application US/09115737
; Patent No. 6348445
; GENERAL INFORMATION:
; APPLICANT: U. Prasad Kari
; Michael McLane
; Taffy J. Williams
; TITLE OF INVENTION: Biologically Active Peptides With Reduced
; Toxicity in Animals and a Method for Preparing Same
; NUMBER OF SEQUENCES: 156
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Finnegan, Henderson, Farabow, Garrett &
; Dunner, L.L.P.
; STREET: 1300 I Street, N.W. Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.3
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/115,737
; FILING DATE: 15-Jul-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/465,330
; FILING DATE: 05-JUN-1995
; APPLICATION NUMBER: 08/184,462
; FILING DATE: 18-JAN-94
; APPLICATION NUMBER: 07/891,201
; FILING DATE: 01-JUN-92
; ATTORNEY/AGENT INFORMATION:
; NAME: Fordie, Jean B
; REGISTRATION NUMBER: 32,984
; REFERENCE/DOCKET NUMBER: 05387.0021-06000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 408-4000
; TELEFAX: (202) 408-4400
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-09-115-737-129

Query Match 50.0%; Score 23; DB 4; Length 10;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 KUKSOLVKR 9
Db 1 KUKKFKLK 9

RESULT 3
US-08-666-564-50
; Sequence 50, Application US/08666564

; Patent No. 5965536
; GENERAL INFORMATION:
; APPLICANT: Cohen, Allen B.
; APPLICANT: Miller, Edmund J.
; APPLICANT: Kurodawa, Anna
; APPLICANT: Hayashi, Shinichiro
; APPLICANT: Tuttle, Ronald R.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CXC INTERCRINE
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,564
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12245
; FILING DATE: 15-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSN:016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 50:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-666-564-50

Query Match 47.8%; Score 22; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 1 KUKSOLVK 8
Db 1 ELRSQSIK 8

RESULT 4
US-08-865-472-50
; Sequence 50, Application US/08865472
; Patent No. 6110889
; GENERAL INFORMATION:
; APPLICANT: Miller, Edmund J.
; APPLICANT: Hayashi, Shinichiro
; TITLE OF INVENTION: PEPTIDE TUMOR CELL GROWTH INHIBITORS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/865,472
FILING DATE: CONCURRENTLY HEREWITH
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/666,564
FILING DATE: 14-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSN:020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-865-472-50

Query Match 47.8%; Score 22; DB 3; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLKSQLVK 8
DB 1 ELRSQSIR 8

RESULT 5
US-09-650-438-50
Sequence 50, Application US/09650438
Patent No. 635619
GENERAL INFORMATION:
APPLICANT: Miller, Edmund J.
HAYASHI, Shinichiro
TITLE OF INVENTION: PEPTIDE TUMOR CELL GROWTH INHIBITORS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/650,438
FILING DATE: 29-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/865,472
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSN:020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-650-438-50

Query Match 47.8%; Score 22; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLKSQLVK 8
DB 1 ELRSQSIR 8

RESULT 6
PCT-US93-12245-50
Sequence 50, Application PC/TUS9312245
GENERAL INFORMATION:
APPLICANT:
APPLICANT: COHEN, Allen B.
APPLICANT: MILLER, Edmund J.
APPLICANT: KUDOWSKA, Anna
APPLICANT: HAYASHI, Shinichiro
APPLICANT: TUTTLE, Ronald R.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CXC
TITLE OF INVENTION: INTERCRINE MOLECULES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12245
FILING DATE: Concurrently herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTFN016PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-12245-50

Query Match 47.8%; Score 22; DB 5; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 KLKSQLVK 8
DB 1 ELRSQSIR 8

RESULT 7
US-08-459-064B-29
Sequence 29, Application US/08459064B
Patent No. 5747452
GENERAL INFORMATION:
APPLICANT: RUOSIAHTI, ERKKI I.

APPLICANT: MORLA, ALEX
TITLE OF INVENTION: A METHOD OF MODULATING TUMOR CELL MIGRATION
TITLE OF INVENTION: USING FIBRONECTIN TYPE III PEPTIDES
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 LA JOLLA VILLAGE DRIVE, STE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,064B
FILING DATE: 01-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,462
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,626
FILING DATE: 16-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/340,812
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1543
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-064B-29

Query Match 45.7%; Score 21; DB 1; Length 9;
Best Local Similarity 71.4%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 KSOVLR 9
Db 1 KSDLVPR 7

RESULT 8
US-08-460-421A-29
Sequence 29, Application US/08460421A
Patent No. 5837813
GENERAL INFORMATION:
APPLICANT: RUOSLAHTI, ERKKI I.
APPLICANT: MORLA, ALEX
TITLE OF INVENTION: FIBRONECTIN BINDING SITES AND METHODS OF
TITLE OF INVENTION: MODULATING FIBRONECTIN EXTRACELLULAR MATRIX ASSEMBLY
NUMBER OF SEQUENCES: 35
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAMPBELL & FLORES LLP
STREET: 4370 LA JOLLA VILLAGE DRIVE, STE 700
CITY: SAN DIEGO
STATE: CALIFORNIA
COUNTRY: UNITED STATES
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,421A
FILING DATE: 01-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/829,462
FILING DATE: 31-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,626
FILING DATE: 16-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/340,812
FILING DATE: 17-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATRYN A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LA 1542
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-9001
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-421A-29

Query Match 45.7%; Score 21; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 3 KSOVLR 9
Db 1 KSDLVPR 7

RESULT 9
US-08-467-202-2
Sequence 2, Application US/08467202
Patent No. 5840295
GENERAL INFORMATION:
APPLICANT: Schwartz, Michal
APPLICANT: Eitan, Shoshana
TITLE OF INVENTION: Enzymatically-Produced Dimeric IL-2 and A
TITLE OF INVENTION: Nerve-Derived Transglutaminase Enzyme for Its Preparation
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Keck, Mahin & Cate
STREET: P.O. Box 06110
CITY: Chicago
STATE: IL
COUNTRY: USA
ZIP: 60606-0110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,202
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/099,759
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/840,783
FILING DATE: 24-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/573,580

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; FILING DATE: 27-AUG-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 102686
; FILING DATE: 30-JUL-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 103469
; FILING DATE: 20-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: IL 105752
; FILING DATE: 19-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Watson T. Scott
; REGISTRATION NUMBER: 26,581
; REFERENCE/DOCKET NUMBER: 47142-053
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 789-3458
; TELEFAX: (202) 789-1158
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-467-202-2

Query Match 45.7%; Score 21; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 SOLVRRK 10
Db 2 SKLTKKK 8

RESULT 10
US-08-666-564-51
; Sequence 51, Application US/08666564
; Patent No. 5965536
; GENERAL INFORMATION:
; APPLICANT: Cohen, Allen B.
; APPLICANT: Miller, Edmund J.
; APPLICANT: Kurdowska, Anna
; APPLICANT: Hayashi, Shinichiro
; APPLICANT: Tuttle, Ronald R.
; TITLE OF INVENTION: PEPTIDE INHIBITORS OF CXC INTERCRINE
; TITLE OF INVENTION: MOLECULES
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/666,564
; FILING DATE: 14-JUN-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/12245
; FILING DATE: 15-DEC-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSN:016
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
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; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-666-564-51

Query Match 45.7%; Score 21; DB 3; Length 10;
Best Local Similarity 37.5%; Pred. No. 4.7e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KXKSQLYR 8
Db 1 ELRWQWIK 8

RESULT 11
US-08-865-472-51
; Sequence 51, Application US/08865472
; Patent No. 610889
; GENERAL INFORMATION:
; APPLICANT: Miller, Edmund J.
; APPLICANT: Hayashi, Shinichiro
; TITLE OF INVENTION: PEPTIDE TUMOR CELL GROWTH INHIBITORS
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/865,472
; FILING DATE: CONCURRENTLY HERewith
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/666,564
; FILING DATE: 14-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Kitchell, Barbara S.
; REGISTRATION NUMBER: 33,928
; REFERENCE/DOCKET NUMBER: UTSN:020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
US-08-865-472-51

Query Match 45.7%; Score 21; DB 3; Length 10;
Best Local Similarity 37.5%; Pred. No. 4.7e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 KXKSQLYR 8
Db 1 ELRWQWIK 8

RESULT 12
US-09-650-438-51
; Sequence 51, Application US/09650438
; Patent No. 6355619
```

GENERAL INFORMATION:
APPLICANT: MILLER, Edmund J.
HAYASHI, Shinichiro
TITLE OF INVENTION: PEPTIDE TUMOR CELL GROWTH INHIBITORS
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/650,438
FILING DATE: 29-AUG-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/865,472
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Kitchell, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSN:020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-650-438-51
Query Match 45.7%; Score 21; DB 4; Length 10;
Best Local Similarity 37.5%; Pred. No. 4.7e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 KLKSQLVK 8
:|:|:|
Db 1 ELRMQMik 8
RESULT 13
PCT-US93-12245-51
Sequence 51, Application PC/TUS9312245
GENERAL INFORMATION:
APPLICANT:
APPLICANT: COHEN, Allen B.
APPLICANT: MILLER, Edmund J.
APPLICANT: KUDOMSKA, Anna
APPLICANT: HAYASHI, Shinichiro
APPLICANT: TUTTLE, Ronald R.
TITLE OF INVENTION: PEPTIDE INHIBITORS OF CXC
TITLE OF INVENTION: INTERCRINE MOLECULES
NUMBER OF SEQUENCES: 58
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/12245
FILING DATE: Concurrently herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: KITCHELL, Barbara S.
REGISTRATION NUMBER: 33,928
REFERENCE/DOCKET NUMBER: UTSN016PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 320-7200
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-12245-51
Query Match 45.7%; Score 21; DB 5; Length 10;
Best Local Similarity 37.5%; Pred. No. 4.7e+02;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 KLKSQLVK 8
:|:|:|
Db 1 ELRMQMik 8
RESULT 14
5514565-10
Patent No. 5514565
APPLICANT: SCHWARTZ, MICHAEL; EITAN, SHOSHANA
TITLE OF INVENTION: ENZYMATICALLY-PRODUCED DIMERIC IL-2
AND A NERVE-DERIVED TRANSGLUTAMINASE ENZYME FOR ITS PREPARATION
NUMBER OF SEQUENCES: 10
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/99,759
FILING DATE: 30-JUL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 840,783
FILING DATE: 24-FEB-1992
APPLICATION NUMBER: 573,580
FILING DATE: 27-AUG-1990
SEQ ID NO: 10:
LENGTH: 10
5514565-10
Query Match 45.7%; Score 21; DB 6; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.7e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 4 SQLVKK 10
:|:|:|
Db 2 SKLVKK 8
RESULT 15
US-08-672-610A-3
Sequence 3, Application US/08672610A
Patent No. 5846933
GENERAL INFORMATION:
APPLICANT: Ziwel, Hwang
APPLICANT: Kottgold, Robert
TITLE OF INVENTION: CD4-DERIVED PEPTIDES THAT INHIBIT IMMUNE
TITLE OF INVENTION: RESPONSES
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York

STATE: New York
COUNTRY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,610A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Friebe, Thomas E.
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8666-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-672-610A-3

Query Match 43.5%; Score 20; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 2e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 KXKSQLVK 8
Db 1 KXSNOLIK 8

Search completed: February 8, 2003, 11:04:42
Job time : 15 secs

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